

```
QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
DE |||||||N|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 4
AAID14444
ID AAD14444 standard; DNA; 25 BP.
XX
AC AAD14444;
XX
XX 01-NOV-2001 (first entry)
XX
DE Recombination site attP2,P3 DNA.
XX
KW Recombination site; copy number; replicon; recombinatorial cloning;
XX attP2,P3; ds.
XX
OS Unidentified.
XX
PN US6270969-B1.
XX
PD 07-AUG-2001.
XX
PF 20-JAN-1999; 99US-0233492.
XX
PR 07-JUN-1996; 96US-0663002.
XX 07-JUN-1995; 95US-0486139.
XX
PA (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX WPI; 2001-488248/53.
XX
PT Methods for apposing nucleic acids comprising an expression signal and
PT a gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under
PT conditions for recombination -
XX
PS Claim 14; Column 18; 76pp; English.
XX
XX The invention relates to a method for apposing an expression signal and
XX a gene or partial gene, using recombinatorial cloning. The method
XX incubates nucleic acids comprising the expression signal and the gene/
XX partial gene in the presence of a recombination protein under conditions
XX sufficient to cause recombination and therefore appose the expression
XX signal and the gene or partial gene. The methods are useful for apposing
XX an expression signal and a gene or partial gene using recombinatorial
XX cloning. The methods are also useful for changing vectors, constructing
XX genes for fusion proteins, changing copy number, changing replicons,
XX cloning into phages, and cloning e.g., PCR products (with an attB site
XX at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
XX The methods are highly specific, rapid, and less labour intensive than
XX prior art methods. The present sequence is a recombination site
XX useful for recombination cloning.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
DE |||||||N|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 5
AAF55745
ID AAF55745 standard; DNA; 25 BP.
XX
AC AAF55745;
XX
```

```
XX 12-APR-2001 (first entry)
XX Recombination site attR3.
XX Recombination site; cloning; att; ss.
XX Unidentified.
XX US6171861-B1.
XX 09-JAN-2001.
XX
PF 12-JAN-1998; 98US-0005476.
XX
PR 07-JUN-1996; 96US-0663002.
XX 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX
PT In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host -
XX
PS Claim 25; Column 46; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
DE |||||||N|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 6
AAF55750
ID AAF55750 standard; DNA; 25 BP.
XX
AC AAF55750;
XX
XX 12-APR-2001 (first entry)
XX
DE Recombination site attP2,P3.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.
XX
PN US6171861-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JAN-1998; 98US-0005476.
```


CC comprising a first nucleic acid sequence having a defined sequence
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first
 CC mutated recombination site that removes one or more stop codons from the
 CC recombination site or avoids hairpin formation, the recombination site
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
 CC comprising a first att recombination site comprising a mutation that
 CC enhances recombination specificity; (3) vectors (IV) comprising the
 CC above mentioned nucleic acids; and (4) cells comprising the above
 CC mentioned nucleic acids or (IV). The nucleic acids are used in
 CC engineering a core region of a given recombination site to provide
 CC mutative sites suitable for subcloning reactions. The use of nucleic
 CC acids for obtaining engineered recombination in vitro or in vivo makes
 CC the methods for DNA or RNA subcloning, highly specific, rapid, and
 CC less labour intensive.

XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 9
 AAS14786
 ID AAS14786 standard; DNA; 25 BP.

XX AC AAS14786;
 XX DT 27-FEB-2002 (first entry)
 XX DE Lambda phage Int recombination site core region DNA sequence attR3.

XX Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
 KW syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
 KW recombination; tumour-specific promoter; hypoxic response element; HRE; ss;
 KW tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
 KW cytosolic; gene therapy; Int recombination site core region; attR3;
 KW exclusive recombination.

XX Bacteriophage lambda.
 XX WO200174861-A2.
 XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10250.
 XX 31-MAR-2000; 2000US-193977P.
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

XX Vile RG, Harrington K, Murphy S, Bateman A;
 XX WPI; 2001-656985/75.

XX Recombinant nucleic acid vector for reducing tumour size, has expression
 PT cassette comprises a promoter linked to nucleic acid sequence encoding
 PT a syncytium-inducing polypeptide and flanked on either side by
 PT recombination -

XX Disclosure; Page 42; 84pp; English.

XX The invention relates to a recombinant nucleic acid vector comprising a
 CC first expression cassette, comprising a first promoter operably linked to
 CC a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
 CC as a fusogenic membrane glycoprotein) and flanked on either side by a
 CC sequence recognised by a recombinase, and/or a second expression cassette

CC comprising a tumour-specific promoter operably linked to a nucleic acid
 CC sequence encoding a recombination. The nucleic acid of the first expression
 CC cassette may be linked to a hypoxic response element (HRE), the second
 CC expression cassette may contain a promoter linked to a nucleic acid
 CC encoding a cytokine, and a third cassette may contain a tumour specific
 CC promoter linked to the nucleic acid encoding the recombination. The tumour
 CC specific promoter is, for example, a carcinoembryonic antigen (CEA)
 CC promoter or a tyrosinase promoter and the recombination is, for example,
 CC Cre recombination or FLP recombination. The invention is useful for reducing
 CC tumour size by administering the compositions as retroviral vectors, or
 CC in a cell containing the vector, to an individual in need of treatment
 CC for a disease caused by malignant cells. This sequence represents an Int
 CC recombination site core region attR3, required for exclusive recombination.

XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 23; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 10
 ABQ82123
 ID ABQ82123 standard; DNA; 25 BP.

XX AC ABQ82123;
 XX DT 11-DEC-2002 (first entry)
 XX DE Core sequence of recombination site attR3 SEQ ID NO:6.

XX Chimeric nucleic acid construct; recombinational cloning; silencing;
 KW recombination site; double stranded RNA; plant; ss.

XX Synthetic.
 XX WO200259294-A1.
 XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-AU00073.
 XX 26-JAN-2001; 2001US-264067P.
 XX 29-NOV-2001; 2001US-333743P.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Wesley S, Waterhouse P, Helliwell C;
 XX WPI; 2002-692669/73.

XX New vectors comprising operably linked DNA fragments having an origin
 PT of replication, a selectable marker and a chimeric DNA construct,
 PT useful for silencing target nucleic acids and for producing large
 PT amounts of double-stranded RNA -

XX Disclosure; Page 15; 104pp; English.

XX The present invention describes a vector (i) comprising operably linked
 CC DNA fragments having: (a) origin of replication allowing replication in a
 CC recipient cell, preferably in bacteria such as Escherichia coli;
 CC (b) selectable marker region capable of being expressed in the recipient
 CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
 CC promoter region capable of being recognized by RNA polymerases of a
 CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
 CC third and fourth recombination sites; (iii) 3' transcription terminating
 CC and polyadenylation region functional in the eukaryotic cell. The first
 CC and fourth recombination sites, or the second and third recombination
 CC sites are capable of reacting with a same recombination site, and

CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
SQ

Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 11

ABQ82128
ID ABQ82128 standard; DNA; 25 BP.

XX
AC ABQ82128;

XX
DT 11-DEC-2002 (first entry)

XX
DE Core sequence of recombination site attP2,P3 SEQ ID NO:11.

XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ss.

OS Synthetic.

XX
FN WO200259294-A1.

XX
PD 01-AUG-2002.

XX
PF 24-JAN-2002; 2002WO-AU00073.

XX
PR 26-JAN-2001; 2001US-264067P.

XX
PR 29-NOV-2001; 2001US-333743P.

XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX
PI Wesley S, Waterhouse P, Helliwell C;

XX
PI WPI; 2002-682669/73.

XX
DR New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -

XX
PS Claim 12; Page 15; 104pp; English.

XX
PS The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerases of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or

CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
SQ

Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 12

ACC44660
ID ACC44660 standard; DNA; 25 BP.

XX
AC ACC44660;

XX
DT 29-MAY-2003 (first entry)

XX
DE Recombination site related oligonucleotide SEQ ID NO:51.

XX
KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; PCR primer; ss.

OS Synthetic.

XX
FN WO200297059-A2.

XX
PD 05-DEC-2002.

XX
PF 30-MAY-2002; 2002WO-US17452.

XX
PR 30-MAY-2001; 2001US-294758P.

XX
PR 21-MAR-2002; 2002US-366891P.

XX
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX
PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;

XX
PI WPI; 2003-140461/13.

XX
DR Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest -

XX
PS Claim 43; Page 143; 272pp; English.

XX
PS The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (i) a platform artificial chromosome
CC expression system (ACes) (ii) comprising several sites that participate
CC in recombine catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or

CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTCTTGTTACAAAGTTGG 25

RESULT 13
 ACC44665
 ID ACC44665 standard; DNA; 25 BP.

AC ACC44665;

XX 29-MAY-2003 (first entry)

DE Recombination site related oligonucleotide SEQ ID NO:56.

XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
 KW art site; integrase; recombinase; ACes; gene therapy; transgenic animal;
 XW platform artificial chromosome expression system; PCR primer; ss.

XX Synthetic.

XX WO200297059-A2.

XX 05-DEC-2002.

XX 30-MAY-2002; 2002WO-US17452.

XX 30-MAY-2001; 2001US-294759P.

PR 21-MAR-2002; 2002US-366891P.

XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 PI Stewart S, Shellard J;

XX WPI; 2003-140461/13.

XX Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest -

XX Claim 43; Page 143; 272pp; English.

XX The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (II) is useful for producing a
 CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic

CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTCTTGTTACAAAGTTGG 25

RESULT 14
 ABT16630

ID ABT16630 standard; DNA; 25 BP.

XX ABT16630;

XX 03-APR-2003 (first entry)

XX Artificial plant chromosome related oligo SEQ ID No 42.

XX Plant artificial chromosome; PAC; transgenic plant; vaccine;

KW blood factor; herbicide; stress; agronomical; nutrient quality;

KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.

XX Unidentified.

XX WO200296923-A1.

XX 05-DEC-2002.

XX 30-MAY-2002; 2002WO-US17451.

XX 30-MAY-2001; 2001US-294687P.

PR 04-JUN-2001; 2001US-296329P.

XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX (AGRI-) AGRISOMA INC.

XX Perez C, Fabijanski SF, Perkins E;

XX WPI; 2003-140436/13.

XX Producing artificial chromosome by introducing a nucleic acid into
 PT plant cell, selecting artificial chromosome that has one or more repeat
 PT regions with equivalent amounts of euchromatic and heterochromatic
 PT nucleic acids -

XX Disclosure; Page 263; 269pp; English.

XX The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rRNA, xDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial

CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for
CC producing plant artificial chromosomes of the invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGTACAAAGTTGG 25
|||||
RESULT 15
ABT16635
ID ABT16635 standard; DNA; 25 BP.
XX AC ABT16635;
XX DT 03-APR-2003 (first entry)
XX DE Artificial plant chromosome related oligo SEQ ID NO 47.
XX KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX OS Unidentified.
XX PN WO200296923-A1.
XX PD 05-DEC-2002.
XX PF 30-MAY-2002; 2002WO-US17451.
XX PR 30-MAY-2001; 2001US-294687P.
XX PR 04-JUN-2001; 2001US-296329P.
XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA (AGRI-) AGRISOMA INC.
XX PI Perez C, Fabijanski SF, Perkins E;
XX WPI; 2003-140436/13.
XX DR
XX PT Producing artificial chromosome by introducing a nucleic acid into
PT plant cell, selecting artificial chromosome that has one or more repeat
PT regions with equivalent amounts of euchromatic and heterochromatic
PT nucleic acids -
XX PS Disclosure; Page 263; 269pp; English.
XX CC The invention relates to a novel method for producing plant artificial
CC chromosomes. The invention also relates to methods for targeting
CC insertion of heterologous DNA into plant artificial chromosomes, methods
CC for delivery of plant chromosomes to selected cells and tissues. The
CC isolated plant artificial chromosome (PAC) is useful for producing a
CC transgenic plant, which involves introducing the PAC into a plant cell.
CC The PAC comprises a heterologous nucleic acid encoding a gene product
CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
CC cytokines, growth factors, antibodies, or a product that provides for
CC resistance to diseases, insects, herbicides, or stress in a plant. The
CC heterologous nucleic acid optionally encodes a product that provides an
CC agronomically important trait in the plant, e.g. a product that alters
CC nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for

CC producing plant artificial chromosomes of the invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGTACAAAGTTGG 25
|||||
RESULT 16
AAS06183
ID AAS06183 standard; DNA; 27 BP.
XX AC AAS06183;
XX DT 12-SEP-2001 (first entry)
XX DE Phage-lambda recombination site attP2.
XX KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
KW lambda integrase; therapeutic; ss.
XX OS Bacteriophage lambda.
XX PN WO200142509-A1.
XX PD 14-JUN-2001.
XX PF 11-DEC-2000; 2000WO-US33546.
XX PR 10-DEC-1999; 99US-0169983.
XX PR 09-MAR-2000; 2000US-0188020.
XX PA (CHRO/) CHEO D.
PA (BRAS/) BRASCH M A.
PA (TEMP/) TEMPLE G F.
PA (HART/) HARTLEY J L.
PA (BYRD/) BYRD D R N.
XX PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX DR
XX PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
PT polypeptides, by mixing the same or different nucleic acids having one
PT or more recombination sites in the presence of recombination proteins,
PT e.g. Cre -
XX PS Disclosure; Fig 24A; 357pp; English.
XX CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination
CC site nucleic acid sequences, and PCR primers of the invention. The
CC att sequences are recognised by the recombination protein lambda
CC integrase (Int). The invention is a new method of producing a population
CC of hybrid nucleic acids comprising mixing at least a first population of
CC nucleic acids comprising one or more recombination sites with at least
CC one target nucleic acid comprising one or more recombination sites and
CC causing some or all of the nucleic acids to recombine with all or some of
CC the target nucleic acids. The method is useful for producing a population
CC of hybrid nucleic acids which may be the same or different. The nucleic
CC acids may be used to express therapeutic proteins or peptides and they
CC may also be used to create novel fusion proteins by expressing different
CC sequences linked to each other. The method allows simultaneous cloning of
CC two or more different nucleic acids.
XX
SQ Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
 |||||

RESULT 17
 ABZ58736
 ID ABZ58736 standard; DNA; 27 BP.
 XX
 AC ABZ58736;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE Att site nucleotide sequence attP2.
 XX
 KW Nucleic acid insertion; recombination; nucleic acid selection;
 KW nucleic acid isolation; att; ds.
 XX
 OS Synthetic.
 XX
 PN WO200295055-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 21-MAY-2002; 2002WO-US15947.
 XX
 PR 21-MAY-2001; 2001US-291973P.
 XX
 PA (INVT-) INVITROGEN CORP.
 XX
 PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
 XX
 DR WPI; 2003-129436/12.
 XX
 PT Inserting a population of nucleic acids into a second target molecule
 PT for selecting and isolating nucleic acid molecules by mixing the second
 PT population of nucleic acid with a second target nucleic acid -
 XX
 PS Disclosure; Fig 13A; 273pp; English.
 XX
 CC The invention relates to inserting a population of nucleic acids into a
 CC second target molecule. The method involves (a) mixing a first population
 CC of nucleic acid comprising one or more recombination sites with a target
 CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
 CC the first population to recombine with the first target nucleic acid
 CC molecules to form a second population; (c) mixing the second population
 CC of nucleic acid with a second target nucleic acid; and (d) causing some
 CC or all of the nucleic acid molecules of the second population to
 CC recombine with some or all of the second target nucleic acid molecules to
 CC form a third population of nucleic acid. The method is useful for
 CC selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
 CC represent att recombination site sequences used in the method of the
 CC invention.
 XX
 SQ Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
 |||||

RESULT 18
 AAC55383/c
 ID AAC55383 standard; DNA; 233 BP.
 XX
 AC AAC55383;
 XX
 DT 11-JAN-2001 (first entry)

11-JAN-2001 (first entry)
 Recombination site nucleotide sequence attP2.
 Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 mutant; recombinational cloning; entry vector; destination vector;
 gene product targeting; fusion tag cleavage; ds.
 Bacteriophage lambda.
 WO200052027-A1.
 08-SEP-2000.
 02-MAR-2000; 2000WO-US05432.
 02-MAR-1999; 99US-0122389.
 23-MAR-1999; 99US-0126049.
 28-MAY-1999; 99US-0136744.
 (LIFE-) LIFE TECHNOLOGIES INC.
 Hartley JL, Brasch MA, Temple GF, Cheo D;
 WPI; 2000-543948/49.
 Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 recombinational cloning of polypeptides -
 Claim 1; Fig 9; 459pp; English.
 The present invention describes isolated nucleic acid molecules (I)
 encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 nucleotide sequence. Also described are: (1) an isolated nucleic acid
 molecule (II) comprising one or more att recombination sites comprising
 at least one mutation in its core region that increases the specificity
 of interaction between the recombination site and a second att
 recombination site; and (2) an isolated nucleic acid molecule (III)
 comprising one or more mutated att recombination sites comprising at
 least one mutation in its core region that enhances the efficiency of
 recombination between a first nucleic acid molecule comprising the
 mutated att recombination site and a second nucleic acid molecule
 comprising a second recombination site that interacts with the mutated
 att recombination site. (I), (II), (III), primers, vectors and methods
 from the present invention are used for the recombinational cloning of
 nucleic acid molecules. They can be used for changing vectors, targeting
 gene products to intracellular locations, cleaving fusion tags from
 desired proteins, operably linking nucleic acid molecules of interest to
 regulatory genetic sequences, constructing genes for fusion proteins,
 changing copy number, changing replicons, cloning into phages and
 cloning. (I), (II), (III), host cells and vectors can be used in the
 production of polypeptides and antibodies. The present sequence is
 used in the exemplification of the present invention.
 Sequence 233 BP; 94 A; 35 C; 32 G; 72 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCTGTACAAAGTTGG 25
 |||||
 Db 100 GTTCAGCTTCTCTGTACAAAGTTGG 76
 |||||

RESULT 19
 AAC55524/c
 ID AAC55524 standard; DNA; 4165 BP.
 XX
 AC AAC55524;
 XX
 DT 11-JAN-2001 (first entry)

```
XX DE Donor plasmid pDONR204 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05432.
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX PI WPI; 2000-543948/49.
XX DR
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Example 9; Fig 52; 459pp; English.
XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at
XX CC least one mutation in its core region that enhances the efficiency of
XX CC recombination between a first nucleic acid molecule comprising the
XX CC mutated att recombination site and a second nucleic acid molecule
XX CC comprising a second recombination site that interacts with the mutated
XX CC att recombination site. (I), (II), (III), primers, vectors and methods
XX CC from the present invention are used for the recombinational cloning of
XX CC nucleic acid molecules. They can be used for changing vectors, targeting
XX CC gene products to intracellular locations, cleaving fusion tags from
XX CC desired proteins, operably linking nucleic acid molecules of interest to
XX CC regulatory genetic sequences, constructing genes for fusion proteins,
XX CC changing copy number, changing replicons, cloning into phages and
XX CC cloning. (I), (II), (III), host cells and vectors can be used in the
XX CC production of polypeptides and antibodies. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 1 other;

Query Match 100.0%; Score 25; DB 21; Length 4165;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
DB 2209 GTTCAGCTTCTTGTCACAAAGTTGG 2185

RESULT 20
AAC55522/c
ID AAC55522 standard; DNA; 4204 BP.
XX AC AAC55522;
XX AC
XX DT 11-JAN-2001 (first entry)
```

```
XX DE Donor plasmid pDONR202 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05432.
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX PI WPI; 2000-543948/49.
XX DR
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Example 9; Fig 50; 459pp; English.
XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at
XX CC least one mutation in its core region that enhances the efficiency of
XX CC recombination between a first nucleic acid molecule comprising the
XX CC mutated att recombination site and a second nucleic acid molecule
XX CC comprising a second recombination site that interacts with the mutated
XX CC att recombination site. (I), (II), (III), primers, vectors and methods
XX CC from the present invention are used for the recombinational cloning of
XX CC nucleic acid molecules. They can be used for changing vectors, targeting
XX CC gene products to intracellular locations, cleaving fusion tags from
XX CC desired proteins, operably linking nucleic acid molecules of interest to
XX CC regulatory genetic sequences, constructing genes for fusion proteins,
XX CC changing copy number, changing replicons, cloning into phages and
XX CC cloning. (I), (II), (III), host cells and vectors can be used in the
XX CC production of polypeptides and antibodies. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 4204 BP; 1198 A; 912 C; 959 G; 1135 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4204;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
DB 2248 GTTCAGCTTCTTGTCACAAAGTTGG 2224

RESULT 21
AAC55523
ID AAC55523 standard; DNA; 4208 BP.
XX AC AAC55523;
XX AC
XX DT 11-JAN-2001 (first entry)
```

```

XX DE Donor plasmid pDONR203 nucleotide sequence.
XX DE
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX PD
XX PD 08-SEP-2000.
XX XX
XX XX 02-MAR-2000; 2000WO-US05432.
XX XX
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX XX
XX XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PA
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX XX
XX DR WPI; 2000-543948/49.
XX XX
XX XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX XX
XX PS Example 9; Fig 51; 459pp; English.
XX XX
XX XX The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at
XX CC least one mutation in its core region that enhances the efficiency of
XX CC recombination between a first nucleic acid molecule comprising the
XX CC mutated att recombination site and a second nucleic acid molecule
XX CC comprising a second recombination site that interacts with the mutated
XX CC att recombination site. (I), (II), (III), primers, vectors and methods
XX CC from the present invention are used for the recombinational cloning of
XX CC nucleic acid molecules. They can be used for changing vectors, targeting
XX CC gene products to intracellular locations, cleaving fusion tags from
XX CC desired proteins, operably linking nucleic acid molecules of interest to
XX CC regulatory genetic sequences, constructing genes for fusion proteins,
XX CC changing copy number, changing replicons, cloning into phages and
XX CC cloning. (I), (II), (III), host cells and vectors can be used in the
XX CC production of polypeptides and antibodies. The present sequence is
XX CC used in the exemplification of the present invention.
XX XX
XX SQ Sequence 4208 BP; 1172 A; 997 C; 875 G; 1164 T; 0 other;
XX
XX Query Match 100.0%; Score 25; DB 21; Length 4208;
XX Best Local Similarity 100.0%; Pred. No. 0.18;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
XX |||||||||||||||||||
XX Db 1291 GTTCAGCTTTCTGTACAAAGTTGG 1315
XX
XX RESULT 22
XX ABZ58768
XX ID ABZ58768 standard; DNA; 4428 BP.
XX AC
XX AC ABZ58768;
XX XX
XX XX 01-MAY-2003 (first entry)
XX DT

```

```

XX DE Destination plasmid pDONR212 nucleotide sequence.
XX DE
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KW nucleic acid isolation; ds.
XX OS
XX OS Synthetic.
XX PN WO200295055-A2.
XX XX
XX XX 28-NOV-2002.
XX XX
XX XX 21-MAY-2002; 2002WO-US15947.
XX XX
XX XX 21-MAY-2001; 2001US-291973P.
XX XX
XX XX (INVI-) INVITROGEN CORP.
XX XX
XX XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX XX
XX XX WPI; 2003-129436/12.
XX XX
XX XX Inserting a population of nucleic acids into a second target molecule
XX PT for selecting and isolating nucleic acid molecules by mixing the second
XX PT population of nucleic acid with a second target nucleic acid -
XX XX
XX PS Disclosure; Fig 27B-C; 273pp; English.
XX XX
XX XX The invention relates to inserting a population of nucleic acids into a
XX CC second target molecule. The method involves (a) mixing a first population
XX CC of nucleic acid comprising one or more recombination sites with a target
XX CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX CC the first population to recombine with the first target nucleic acid
XX CC molecules to form a second population; (c) mixing the second population
XX CC of nucleic acid with a second target nucleic acid; and (d) causing some
XX CC or all of the nucleic acid molecules of the second population to
XX CC recombine with some or all of the second target nucleic acid molecules to
XX CC form a third population of nucleic acid. The method is useful for
XX CC selecting and isolating nucleic acid molecules. The present sequence
XX CC represents the destination plasmid pDONR212 nucleotide sequence.
XX XX
XX SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 other;
XX
XX Query Match 100.0%; Score 25; DB 25; Length 4428;
XX Best Local Similarity 100.0%; Pred. No. 0.18;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
XX |||||||||||||||||||
XX Db 3180 GTTCAGCTTTCTGTACAAAGTTGG 3204
XX
XX RESULT 23
XX AAC55521
XX ID AAC55521 standard; DNA; 4470 BP.
XX XX
XX AC AAC55521;
XX XX
XX DT 11-JAN-2001 (first entry)
XX XX
XX DE Donor plasmid pDONR201 nucleotide sequence.
XX XX
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX XX
XX XX Bacteriophage lambda.
XX OS
XX OS Synthetic.
XX XX
XX XX WO200052027-A1.
XX PN
XX XX
XX PD 08-SEP-2000.
XX XX

```


PF 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
DR
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
XX Example 9; Fig 49; 459pp; English.
PS
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III) primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX
XX Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 21; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;
QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
DB 2343 GTTCAGCTTCTTGTTACAAAGTTGG 2367
RESULT 24
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
AC ABZ58767;
XX
XX 01-MAY-2003 (first entry)
DT
XX Destination plasmid pDONR201 nucleotide sequence.
DE
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
PN
XX 28-NOV-2002.
PD
XX 21-MAY-2002; 2002WO-US15947.
PF
XX 21-MAY-2003 (first entry)
XX
XX Destination plasmid pDONR201 nucleotide sequence.
DE
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
PN
XX 28-NOV-2002.
PD
XX 21-MAY-2002; 2002WO-US15947.
PF
XX
XX

PR 21-MAY-2001; 2001US-291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
XX WPI; 2003-129436/12.
DR
XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -
XX
XX Disclosure; Fig 26B-C; 273pp; English.
PS
XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR201 nucleotide sequence.
XX
XX Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 25; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;
QY 1 GTTCAGCTTCTTGTTACAAAGTTGG 25
DB 2343 GTTCAGCTTCTTGTTACAAAGTTGG 2367
RESULT 25
ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.
XX
AC ABZ58769;
XX
XX 01-MAY-2003 (first entry)
DT
XX Destination plasmid pDONR212(F) nucleotide sequence.
DE
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
PN
XX 28-NOV-2002.
PD
XX 21-MAY-2002; 2002WO-US15947.
PF
XX 21-MAY-2003; 2001US-291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
XX WPI; 2003-129436/12.
DR
XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -
XX
XX Disclosure; Fig 26B-C; 273pp; English.
PS
XX

CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(F) nucleotide sequence.

XX SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGATACAAAGTTGG 25
Db 2331 GTTCAGCTTCTTGATACAAAGTTGG 2355

RESULT 26
ABZ58770
ID ABZ58770 standard; DNA; 4627 BP.
XX AC ABZ58770;
XX DT 01-MAY-2003 (first entry)
XX DE Destination plasmid pDONR212(R) nucleotide sequence.
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KW nucleic acid isolation; ds.
XX OS Synthetic.
XX XN WO200295055-A2.
XX PD 28-NOV-2002.
XX PF 21-MAY-2002; 2002WO-US:5947.
XX PR 21-MAY-2001; 2001US-291973P.
XX PA (INVI-) INVITROGEN CORP.

XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX NPI; 2003-129436/12.
XX PT Inserting a population of nucleic acids into a second target molecule
XX for selecting and isolating nucleic acid molecules by mixing the second
XX population of nucleic acid with a second target nucleic acid -
XX PS Disclosure; Fig 29B-C; 273pp; English.
XX CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(R) nucleotide sequence.

XX SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGATACAAAGTTGG 25
Db 2331 GTTCAGCTTCTTGATACAAAGTTGG 2355

RESULT 27
AAC55525
ID AAC55525 standard; DNA; 4939 BP.
XX AC AAC55525;
XX DT 11-JAN-2001 (first entry)
XX DE Donor plasmid pDONR205 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attL; attR;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
XX OS Synthetic.

XX PN WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05432.
XX PR 02-MAR-1999; 99US-0122389.
XX PR 23-MAR-1999; 99US-0126049.
XX PR 28-MAY-1999; 99US-0136744.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX NPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides -

XX Example 10; Fig 53; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX att recombination site. (I), (II), (III), primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is
XX used in the exemplification of the present invention.

XX SQ Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4939;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||
Db 938 GTTCAGCTTTCTGTACAAAGTTGG 962

RESULT 28
AAC5525/c
ID AAC5526 standard; DNA; 5156 BP.

XX AC AAC5526;

XX DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR206 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
XX OS Synthetic.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides -

XX Example 9; Fig 54; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
nucleotide sequence. Also described are: (1) an isolated nucleic acid
molecule (II) comprising one or more att recombination sites comprising
at least one mutation in its core region that increases the specificity
of interaction between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (I), (II), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning. (I), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is
used in the exemplification of the present invention.

XX Sequence 5156 BP; 1413 A; 1183 C; 1216 G; 1342 T; 2 other;

Query Match 100.0%; Score 25; DB 21; Length 5156;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||
Db 3200 GTTCAGCTTTCTGTACAAAGTTGG 3176

RESULT 29
AAC55632/c

ID AAC55632 standard; DNA; 5584 BP.

XX AC AAC55632;

XX DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR207 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
XX OS Synthetic.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides -

XX Disclosure; Fig 97; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
nucleotide sequence. Also described are: (1) an isolated nucleic acid
molecule (II) comprising one or more att recombination sites comprising
at least one mutation in its core region that increases the specificity
of interaction between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (I), (II), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning. (I), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is
used in the exemplification of the present invention.

XX Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
|||||
Db 3243 GTTCAGCTTTCTTGTCACAAAGTTGG 3219

RESULT 30
ABZ58766/C
ID ABZ58766 standard; DNA; 5584 BP.
XX
AC ABZ58766;
XX
DT 01-MAY-2003 (first entry)
XX
DE Donor plasmid pDONR207 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WC200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US15947.
XX
PR 21-MAY-2001; 2001US-291973P.
XX

(INVI-) INVITROGEN CORP.

XX
XX Bransch MA, Cheo D, Li X, Esposito D, Byrd DRN;
PI WPI; 2003-129436/12.
XX

XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -
XX

XX Disclosure; Fig 18B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence.

XX SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
|||||
Db 3243 GTTCAGCTTTCTTGTCACAAAGTTGG 3219

RESULT 31
ABQ82130
ID ABQ82130 standard; DNA; 18691 BP.
XX

AC ABQ82130;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.

XX WO200259294-A1.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-AU00073.

XX 26-JAN-2001; 2001US-264067P.

XX 29-NOV-2001; 2001US-333743P.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Mesley S, Waterhouse P, Helliwell C;

XX WPI; 2002-682669/73.

XX New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX

XX Claim 13; Page 62-72; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerases of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC an acceptor vector nucleotide sequence from the present invention.

XX SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
|||||
Db 14520 GTTCAGCTTTCTTGTCACAAAGTTGG 14544

RESULT 32
ABQ82130/C
ID ABQ82130 standard; DNA; 18691 BP.
XX
AC ABQ82130;
XX

DT 11-DEC-2002 (first entry)
 DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.
 XX Chimeric nucleic acid construct; recombinational cloning; silencing;
 XX recombination site; double stranded RNA; plant; ds.
 KW Synthetic.
 OS WO200259294-A1.
 XX 01-AUG-2002.
 XX 24-JAN-2002; 2002WO-AU00073.
 XX 26-JAN-2001; 2001US-264067P.
 XX 29-NOV-2001; 2001US-333743P.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Wesley S, Waterhouse P, Helliwell C;
 XX WPI; 2002-682669/73.
 XX New vectors comprising operably linked DNA fragments having an origin
 PT of replication, a selectable marker and a chimeric DNA construct,
 PT useful for silencing target nucleic acids and for producing large
 PT amounts of double-stranded RNA -
 XX Claim 13; Page 62-72; 104pp; English.
 XX The present invention describes a vector (I) comprising operably linked
 CC DNA fragments having: (a) origin of replication allowing replication in a
 CC recipient cell, preferably in bacteria such as *Escherichia coli*;
 CC (b) selectable marker region capable of being expressed in the recipient
 CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
 CC promoter region capable of being recognized by RNA polymerase of a
 CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
 CC third and fourth recombination sites; (iii) 3' transcription terminating
 CC and polyadenylation region functional in the eukaryotic cell. The first
 CC and fourth recombination sites, or the second and third recombination
 CC sites are capable of reacting with a same recombination site, and
 CC preferably are identical. The first and second recombination sites, or
 CC the third and fourth recombination sites, do not recombine with each
 CC other or with a same recombination site. The vector is useful for
 CC producing large amounts of double-stranded RNA which can be used for
 CC silencing target nucleic acid sequences. The vectors can also be used to
 CC convert a DNA fragment into an inverted repeat structure. Plants
 CC transformed with a vector from the present invention can be used in a
 CC conventional breeding scheme to produce more plants with the same
 CC characteristics or to introduce a chimeric gene for reduction of the
 CC phenotypic expression of nucleic acids. The present sequence represents
 CC an acceptor vector nucleotide sequence from the present invention.
 XX
 SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;
 Query Match 100.0%; Score 25; DB 24; Length 18691;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
 Db 16418 GTTCAGCTTCTTGACAAAGTTGG 16394
 RESULT 33
 AAX78977
 ID AAX78977 standard; DNA; 25 BP.
 XX AAX78977;
 AC AAX78977;
 XX 17-AUG-1999 (first entry)
 DT 17-AUG-1999 (first entry)
 XX

DE Oligonucleotide #43 for recombination and cloning method.
 XX Cloning; donor; recombination site; vector; chimeric; ss.
 XX Synthetic.
 XX WO9921977-A1.
 XX 06-MAY-1999.
 XX 26-OCT-1998; 98WO-US22589.
 XX 23-OCT-1998; 98US-0177387.
 XX 24-OCT-1997; 97US-0065930.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Brasch MA, Fox DK, Hartley JL, Temple GF;
 XX WPI; 1999-303011/25.
 XX New nucleic acid cloning methods
 XX Disclosure; Page 171; 185pp; English.
 XX The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NMs) comprising: (a) combining in vitro or
 CC in vivo: (i) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that
 CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX
 SQ Sequence 25 BP; 4 A; 3 C; 5 G; 10 T; 3 other;
 Query Match 95.2%; Score 23.8; DB 20; Length 25;
 Best Local Similarity 88.0%; Pred. No. 0.37;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
 Db 1 GTTCAGCTTCTTGACAAAGTTGG 25
 RESULT 34
 AAT48224
 ID AAT48224 standard; DNA; 25 BP.
 XX AAT48224;
 AC AAT48224;
 XX 20-OCT-1997 (first entry)
 DT 20-OCT-1997 (first entry)
 XX attP1 core region.
 DE attP1 core region.
 XX att recombination site; core region; mutation; enhance; recombination;
 KW vector; subcloning; regulation; exchange; ss.
 XX Synthetic.
 OS WO9640724-A1.
 XX 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US10082.
 XX

PR 07-JUN-1995; 95US-0486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Brasch MA, Hartley JL;
 XX WPI; 1997-065168/06.
 DR
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in
 PT vitro or in vivo
 XX
 XX Claim 14; Page 56; 106pp; English.
 XX
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA.
 XX
 XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 SQ
 Query Match 93.6%; Score 23.4; DB 18; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.56;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
 Db 1 GTTCAGCTTCTTGACAAAGTTGG 25
 XX
 RESULT 35
 AAX78949
 ID AAX78949 standard; DNA; 25 BP.
 XX
 XX AAX78949;
 XX
 XX 17-AUG-1999 (first entry)
 DT
 XX
 XX Oligonucleotide #15 for recombination and cloning method.
 DE
 XX Cloning; donor; recombination site; vector; chimeric; ss.
 KW
 XX Synthetic.
 OS
 XX WO9921977-A1.
 PN
 XX
 XX 06-MAY-1999.
 PD
 XX 26-OCT-1998; 98WO-US22589.
 PF
 XX 23-OCT-1998; 98US-0177387.
 PR
 XX 24-OCT-1997; 97US-0065930.
 PR
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA
 XX Brasch MA, Fox DK, Hartley JL, Temple GF;
 PI
 XX WPI; 1999-303011/25.
 DR
 XX New nucleic acid cloning methods
 PT
 XX Disclosure; Page 162; 185pp; English.
 PS
 XX The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or

CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that
 CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX
 XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 SQ
 Query Match 93.6%; Score 23.4; DB 20; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.56;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
 Db 1 GTTCAGCTTCTTGACAAAGTTGG 25
 XX
 RESULT 36
 AAD14443
 ID AAD14443 standard; DNA; 25 BP.
 XX
 XX AAD14443;
 XX
 XX 01-NOV-2001 (first entry)
 DT
 XX
 XX Recombination site attP1 DNA.
 DE
 XX Recombination site; copy number; replicon; recombinatorial cloning;
 KW attP1; ds.
 XX
 XX Unidentified.
 OS
 XX US6270969-B1.
 FN
 XX 07-AUG-2001.
 PD
 XX 20-JAN-1999; 99US-0233492.
 PF
 XX 07-JUN-1996; 96US-0663002.
 PR
 XX 07-JUN-1995; 95US-0486139.
 PR
 XX (INVI-) INVITROGEN CORP.
 PA
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 2001-488248/53.
 DR
 XX
 XX Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 XX
 XX Claim 14; Column 18; 76pp; English.
 PS
 XX The invention relates to a method for apposing an expression signal and
 CC a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 CC partial gene in the presence of a recombination protein under conditions
 CC sufficient to cause recombination and therefore appose the expression
 CC signal and the gene or partial gene. The methods are useful for apposing
 CC an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.

CC The methods are highly specific, rapid, and less labour intensive than
CC prior art methods. The present sequence is a recombination site
CC useful for recombination cloning.

XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
SQ Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.56;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||
DB 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 37
AAF55749
ID AAF55749 standard; DNA; 25 BP.

XX AAF55749;
AC
XX 12-APR-2001 (first entry)
DT Recombination site attP1.
DE
XX Recombination site; cloning; att; ss.
KW
XX Unidentified.
OS
XX US6171861-B1.
FN
XX 09-JAN-2001.

XX 12-JAN-1998; 98US-0005476.
XX 07-JUN-1996; 96US-0663002.
XX 07-JUN-1995; 95US-0486139.
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Hartley JL, Brasch MA;
PI
XX MPI; 2001-136877/14.
DR
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host -
XX Claim 25; Column 46; 73pp; English.

XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention.

XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
SQ Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.56;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||
DB 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 38
AAC87880
ID AAC87880 standard; DNA; 25 BP.
XX
XX AAC87880;
AC
XX 02-MAR-2001 (first entry)
DT
XX Escherichia coli core region recombinant site attP1 SEQ ID NO:15.
DE
XX Core region; recombination site; cloning; chimeric DNA;
KW characteristic; mutation; att site; lox site; ss.
XX
XX Escherichia coli.
OS
XX US6143557-A.
FN
XX 07-NOV-2000.
PD
XX 20-JAN-1999; 99US-0233493.
XX 07-JUN-1996; 96US-0663002.
XX 12-JAN-1998; 98US-0005476.
XX 07-JUN-1995; 95US-0486139.
XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;
PI
XX MPI; 2001-049004/06.
DR
XX Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation -
XX Claim 1; Column 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the
CC above mentioned nucleic acids; and (4) cells comprising the above
CC mentioned nucleic acids or (IV). The nucleic acids are used in
CC engineering a core region of a given recombination site to provide
CC mutative sites suitable for subcloning reactions. The use of nucleic
CC acids for obtaining engineered recombination in vitro or in vivo makes
CC the methods for DNA or RNA subcloning, highly specific, rapid, and
CC less labour intensive.

XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
SQ Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.56;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||
DB 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 39
ABQ82127
ID ABQ82127 standard; DNA; 25 BP.
XX
XX ABQ82127;

XX 11-DEC-2002 (first entry)
XX
DE Core sequence of recombination site attP1 SEQ ID NO:10.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plasmid; ss.
XX
OS Synthetic.
XX
XX WO200259294-A1.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU00073.
XX
XX 26-JAN-2001; 2001US-264067P.
XX
XX 29-NOV-2001; 2001US-333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin
XX of replication, a selectable marker and a chimeric DNA construct,
XX useful for silencing target nucleic acids and for producing large
XX amounts of double-stranded RNA -
XX
XX Claim 12; Page 15; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
XX DNA fragments having: (a) origin of replication allowing replication in a
XX recipient cell, preferably in bacteria such as *Escherichia coli*;
XX (b) selectable marker region capable of being expressed in the recipient
XX cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX promoter region capable of being recognized by RNA polymerases of a
XX eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX third and fourth recombination sites; (iii) 3' transcription terminating
XX and polyadenylation region functional in the eukaryotic cell. The first
XX and fourth recombination sites, or the second and third recombination
XX sites are capable of reacting with a same recombination site, and
XX preferably are identical. The first and second recombination sites, or
XX the third and fourth recombination sites, do not recombine with each
XX other or with a same recombination site. The vector is useful for
XX producing large amounts of double-stranded RNA which can be used for
XX silencing target nucleic acid sequences. The vectors can also be used to
XX convert a DNA fragment into an inverted repeat structure. Plants
XX transformed with a vector from the present invention can be used in a
XX conventional breeding scheme to produce more plants with the same
XX characteristics or to introduce a chimeric gene for reduction of the
XX phenotypic expression of nucleic acids. The present sequence represents
XX the core sequence of recombination site attB1 which is given in the
XX exemplification of the present invention.
XX
XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
XX
XX Query Match 93.6%; Score 23.4; DB 24; Length 25;
XX Best Local Similarity 96.0%; Pred. No. 0.56;
XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTTCAGCTTTCTTTGTACAAAGTTGG 25
XX |||||
XX Db 1 GTTCAGCTTTTTTGTACAAAGTTGG 25

RESULT 40
ACC44664
ID ACC44664 standard; DNA; 25 BP.
XX
XX AC ACC44664;
XX

DT 29-MAY-2003 (first entry)
XX
DE Recombination site related oligonucleotide SEQ ID NO:55.
XX
KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO200297059-A2.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US17452.
XX
XX 30-MAY-2001; 2001US-294758P.
XX
XX 21-MAR-2002; 2002US-366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX Stewart S, Shellard J;
XX
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
XX permits site-directed integration in the presence of lambda-integrase,
XX useful for site-specific recombination-directed integration of DNA of
XX interest -
XX
XX Claim 43; Page 143; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
XX one or several att sites, where an att site is heterologous to the
XX chromosome, and permits site-directed integration in the presence of
XX lambda-integrase. Also described: (1) a platform artificial chromosome
XX expression system (ACes) (II) comprising several sites that participate
XX in recombinase catalyzed recombination; and (2) a method (M1) for
XX introducing a heterologous nucleic acid into a platform artificial
XX chromosome. (I) can be used in gene therapy. (M1) is useful for
XX introducing a heterologous nucleic acid molecule into a platform
XX artificial chromosome, preferably an ACes. (II) is useful for producing a
XX transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
XX mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
XX by a carrier system, microinjection, microcell fusion, electroporation,
XX microprojectile bombardment or direct DNA transfer into an embryonic
XX cell, preferably a stem cell or an embryo. (II) comprises a heterologous
XX nucleic acid that encodes a therapeutic product which is useful for
XX making a library of ACes comprising random portions of a genome. ACC44612
XX to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
XX exemplification of the present invention.
XX
XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
XX
XX Query Match 93.6%; Score 23.4; DB 25; Length 25;
XX Best Local Similarity 96.0%; Pred. No. 0.56;
XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTTCAGCTTTCTTTGTACAAAGTTGG 25
XX |||||
XX Db 1 GTTCAGCTTTTTTGTACAAAGTTGG 25

Search completed: November 6, 2003, 22:26:30
Job time : 112.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 23:06:49 ; Search time 102.25 Seconds
(without alignments)
780.185 Million cell updates/sec

Title: US-10-055-001A-11

Perfect score: 25
Sequence: 1 gttcagctttctgtacaaagtgg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2141354 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	9	US-09-855-797A-16
2	25	100.0	25	10	US-09-822-634-8
3	25	100.0	25	10	US-09-907-900-16
4	25	100.0	25	10	US-09-907-719-16
5	25	100.0	25	11	US-09-432-085-11
6	25	100.0	25	11	US-09-432-085-11
7	25	100.0	25	12	US-09-985-448-16
8	25	100.0	25	12	US-10-300-892-15
9	25	100.0	25	14	US-10-055-001A-11
10	25	100.0	25	14	US-10-055-001A-11
11	25	100.0	25	14	US-10-058-292-11
12	25	100.0	25	14	US-10-058-292-16
13	25	100.0	25	14	US-10-162-879-11
14	25	100.0	25	14	US-10-162-879-16
15	25	100.0	25	14	US-10-161-403-51
16	25	100.0	25	14	US-10-161-403-56

17	25	100.0	27	9	US-09-732-914-10	Sequence 10, Appl	
18	25	100.0	27	14	US-10-151-690-34	Sequence 34, Appl	
19	25	100.0	4428	14	US-10-151-690-62	Sequence 62, Appl	
20	25	100.0	4470	14	US-10-151-690-21	Sequence 21, Appl	
21	25	100.0	4627	14	US-10-151-690-63	Sequence 63, Appl	
22	25	100.0	4627	14	US-10-151-690-64	Sequence 64, Appl	
23	25	100.0	5584	14	US-10-151-690-61	Sequence 61, Appl	
c	24	25	100.0	17862	14	US-10-055-001A-23	Sequence 23, Appl
c	25	25	100.0	17862	14	US-10-055-001A-13	Sequence 13, Appl
c	26	25	100.0	18691	14	US-10-055-001A-13	Sequence 13, Appl
c	27	25	100.0	18691	14	US-10-055-001A-13	Sequence 13, Appl
28	23.8	95.2	25	9	US-09-855-797A-43	Sequence 43, Appl	
29	23.8	95.2	25	10	US-09-907-900-43	Sequence 43, Appl	
30	23.8	95.2	25	10	US-09-907-719-43	Sequence 43, Appl	
31	23.8	95.2	25	12	US-09-985-448-43	Sequence 43, Appl	
32	23.8	95.2	25	12	US-10-300-892-43	Sequence 43, Appl	
33	23.4	93.6	25	9	US-09-855-797A-15	Sequence 15, Appl	
34	23.4	93.6	25	10	US-09-907-900-15	Sequence 15, Appl	
35	23.4	93.6	25	10	US-09-907-719-15	Sequence 15, Appl	
36	23.4	93.6	25	11	US-09-432-085-15	Sequence 15, Appl	
37	23.4	93.6	25	12	US-09-985-448-15	Sequence 15, Appl	
38	23.4	93.6	25	12	US-10-300-892-15	Sequence 15, Appl	
39	23.4	93.6	25	14	US-10-055-001A-10	Sequence 10, Appl	
40	23.4	93.6	25	14	US-10-058-292-15	Sequence 15, Appl	
41	23.4	93.6	25	14	US-10-162-879-15	Sequence 15, Appl	
42	23.4	93.6	25	14	US-10-161-403-55	Sequence 55, Appl	
43	23.4	93.6	27	9	US-09-732-914-6	Sequence 6, Appl	
44	23.4	93.6	27	14	US-10-151-690-30	Sequence 30, Appl	
c	45	23.4	4470	14	US-10-151-690-21	Sequence 21, Appl	

ALIGNMENTS

RESULT 1
US-09-855-797A-16
; Sequence 16, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-16

Query Match 100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0

Qy 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||

RESULT 2


```
US-09-822-634-8
; Sequence 8, Application US/09822634
; Patent No. US2002015056A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
US-09-822-634-8
Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
RESULT 3
US-09-907-900-16
; Sequence 16, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-16
Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
RESULT 4
US-09-907-719-16
; Sequence 16, Application US/09907719
```

```
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-16
Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
RESULT 5
US-09-432-085-11
; Sequence 11, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
```

```
;
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-432-085-11

Query Match      100.0%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
   ||||||||||||||||||||||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 6
US-09-432-085-16
; Sequence 16, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; MOLECULE TYPE: cdna
; US-09-432-085-11

Query Match      100.0%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
   ||||||||||||||||||||||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 7
US-09-985-448-16
; Sequence 16, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-985-448-16

Query Match      100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
   ||||||||||||||||||||||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 8
US-10-300-932-16
; Sequence 16, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
```

TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: Products
US-10-300-892-16

Query Match 100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 9
US-10-055-001A-6
Sequence 11, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
FILE REFERENCE: HELIGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: core sequence of recombination site attR3
US-10-055-001A-6

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 10
US-10-055-001A-11
Sequence 11, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
FILE REFERENCE: HELIGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: core sequence of recombination site attP2,P3
US-10-055-001A-11

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 11
US-10-058-292-11
Sequence 11, Application US/10058292
Publication No. US20030054552A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-058-292-11

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 12
US-10-058-292-16
Sequence 16, Application US/10058292
Publication No. US20030054552A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.

;;
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; Recombination Sites
;;
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/058,292
;; FILING DATE: 30-Jan-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/432,085
;; FILING DATE: 1999-11-02
;; APPLICATION NUMBER: 09/233,493
;; FILING DATE: 20-JAN-1999
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;;
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
;; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-058-292-16

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 13
US-10-162-879-11
; Sequence 11, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996

;;
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/162,879
;; FILING DATE: 06-Jun-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/432,085
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 09/233,493
;; FILING DATE: 20-JAN-1999
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;;
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
;; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-162-879-11

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 14
US-10-162-879-16
; Sequence 16, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996

```
; APPLICATION NUMBER: 08/496,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-162-879-16

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 15
US-10-161-403-51
; Sequence 51, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attR3
US-10-161-403-51

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 16
US-10-161-403-56
; Sequence 56, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attR3
US-10-161-403-51

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 17
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US2002007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attP2
US-09-732-914-10

Query Match      100.0%; Score 25; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 18
US-10-151-690-34
; Sequence 34, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: Brasch, Michael A.
```

```
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attP2,P3
US-10-161-403-56

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 17
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US2002007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attP2
US-09-732-914-10

Query Match      100.0%; Score 25; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 18
US-10-151-690-34
; Sequence 34, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
```

```

; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attp2
US-10-151-690-34

Query Match      100.0%; Score 25; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 19
US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

Query Match      100.0%; Score 25; DB 14; Length 4428;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 3180 GTTCAGCTTCTTGTACAAAGTTGG 3204

RESULT 20
US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID

```

```

; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; OTHER INFORMATION: plasmid pDONR201
US-10-151-690-21

Query Match      100.0%; Score 25; DB 14; Length 4470;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
Db 2343 GTTCAGCTTCTTGTACAAAGTTGG 2367

RESULT 21
US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690

```

; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63

Query Match 100.0%; Score 25; DB 14; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||
Db 2331 GTTCAGCTTTCTGTACAAAGTTGG 2355

RESULT 22

US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US2003012455A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 100.0%; Score 25; DB 14; Length 4627;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||
Db 2331 GTTCAGCTTTCTGTACAAAGTTGG 2355

RESULT 23

US-10-151-690-61/c
; Sequence 61, Application US/10151690
; Publication No. US2003012455A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match 100.0%; Score 25; DB 14; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||
Db 3243 GTTCAGCTTTCTGTACAAAGTTGG 3219

RESULT 24

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match 100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||
Db 14520 GTTCAGCTTTCTGTACAAAGTTGG 14544

RESULT 25

US-10-055-001A-23/c
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA

```

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match      100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
    |||||
Db 15589 GTTCAGCTTTCTTGTCACAAAGTTGG 15565

RESULT 26
US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCES: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE

; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)

; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2146)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13

Query Match      100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
    |||||
Db 14520 GTTCAGCTTTCTTGTCACAAAGTTGG 14544

RESULT 27
US-10-055-001A-13/c
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCES: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)

```



```
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13
```

```
Query Match          100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;
```

```
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
    |||||
Db 16418 GTTCAGCTTCTTGTCACAAAGTTGG 16394
```

RESULT 28

```
US-09-855-797A-43
; Sequence 43, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
```

```
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-855-797A-43
```

```
Query Match          95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
    |||||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
```

RESULT 29

```
US-09-907-900-43
; Sequence 43, Application US/09907900
; Patent No. US2002072997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-907-900-43
```

```
Query Match          95.2%; Score 23.8; DB 10; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
    |||||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
```

RESULT 30

```
US-09-907-719-43
; Sequence 43, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
```

```
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-43
```

```
Query Match          95.2%; Score 23.8; DB 10; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25
```

```
RESULT 31
US-09-985-448-43
; Sequence 43, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/055,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-43
```

```
Query Match          95.2%; Score 23.8; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25
```

```
RESULT 32
US-10-300-892-43
; Sequence 43, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-43
```

```
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-43
```

```
Query Match          95.2%; Score 23.8; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25
```

```
RESULT 33
US-09-855-797A-15
; Sequence 15, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-15
```

```
Query Match          93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTCTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTTRTACAAAGTTGG 25
```

```
RESULT 34
US-09-907-900-15
; Sequence 15, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
```

```
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-15

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 35
US-09-907-719-15
; Sequence 15, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-15

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 36
US-09-432-085-15
; Sequence 15, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
```

```
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/432,085
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-15

Query Match          93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 37
US-09-985-448-15
; Sequence 15, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-15

```

```

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Indels 1; Indels 0; Gaps 0;

```

```

QY 1 GTTCAGCTTTCTTGACAAAGTTGG 25
    |||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

RESULT 38
US-10-300-892-15
; Sequence 15, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-15

```

```

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Indels 1; Indels 0; Gaps 0;

```

```

QY 1 GTTCAGCTTTCTTGACAAAGTTGG 25
    |||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

RESULT 39
US-10-055-001a-10
; Sequence 10, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellmuth, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attP1
US-10-055-001A-10

```

```

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Indels 1; Indels 0; Gaps 0;

```

```

QY 1 GTTCAGCTTTCTTGACAAAGTTGG 25
    |||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

RESULT 40
US-10-058-292-15
; Sequence 15, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-058-292-15

```

```

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.28; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Indels 1; Indels 0; Gaps 0;

```

```

QY 1 GTTCAGCTTTCTTGACAAAGTTGG 25
    |||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

Fri Nov 7 08:08:38 2003

us-10-055-001a-11.rnpb

Page 14

Search completed: November 7, 2003, 02:22:27
Job time : 103.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds
(without alignments)
555,531 Million cell updates/sec

Title: US-10-055-001A-11
Perfect score: 25
Sequence: 1 gttcagctttctgacaaagtgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_esti:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_plg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	22	88.0	87	14	CB400039
c 2	22	88.0	90	14	CB392047
c 3	22	88.0	92	14	CB402537
c 4	22	88.0	94	14	CB402408

c 5	22	88.0	95	14	CB400591	OSTF179E7
c 6	22	88.0	95	14	CB401751	OSTF198G7
c 7	22	88.0	97	14	CB401179	OSTF190A5
c 8	22	88.0	98	14	CB402581	OSTF215C2
c 9	22	88.0	100	14	CB392051	OSTF163A3
c 10	22	88.0	100	14	CB400512	OSTF177G3
c 11	22	88.0	102	14	CB392040	OSTF162H1
c 12	22	88.0	103	14	CB401874	OSTF202B1
c 13	22	88.0	107	14	CB388456	OSTF099E7
c 14	22	88.0	111	14	CB394444	OSTF137H4
c 15	22	88.0	114	14	CB402012	OSTF205B3
c 16	22	88.0	120	14	CB392055	OSTF163B1
c 17	22	88.0	120	14	CB400382	OSTF175B7
c 18	22	88.0	124	14	CB399813	OSTF163C2
c 19	22	88.0	126	14	CB400130	OSTF169C5
c 20	22	88.0	128	14	CB400226	OSTF171D4
c 21	22	88.0	128	14	CB401884	OSTF202C5
c 22	22	88.0	129	14	CB401218	OSTF191C6
c 23	22	88.0	227	14	CB398923	OSTR212B6
c 24	22	88.0	247	14	CB401020	OSTR186E2
c 25	22	88.0	262	14	CB395877	OSTR163A3
c 26	22	88.0	263	14	CB395890	OSTR163C2
c 27	22	88.0	380	12	B1174869	OSTF061D8
c 28	22	88.0	435	12	B1174871	OSTF061E1
c 29	22	88.0	460	12	B1174883	OSTF061F9
c 30	22	88.0	467	12	B1174361	OSTF042E6
c 31	22	88.0	480	12	B1174878	OSTF061F1
c 32	22	88.0	501	12	B1174375	OSTF042G8
c 33	22	88.0	508	12	B1174868	OSTF061D7
c 34	22	88.0	549	12	B1174892	OSTF061G9
c 35	22	88.0	559	14	CB395875	OSTR163A1
c 36	22	88.0	583	12	B1174904	OSTF062B1
c 37	22	88.0	613	12	B1174910	OSTF062B7
c 38	22	88.0	1388	14	CB960041	CB960041 AGENCOURT
c 39	22	84.0	559	9	AL515389	AL515389 AL515389
c 40	21	84.0	982	14	CD048261	CD048261 AGENCOURT
c 41	21	84.0	1097	9	AL515449	AL515449 AL515449
c 42	20.8	83.2	1048	29	CC260943	CC260943 CH261-81B
c 43	20.6	82.4	959	9	AL514767	AL514767 AL514767
c 44	20.6	82.4	1201	9	AL513677	AL513677 AL513677
c 45	20.6	82.4	1201	9	AL514171	AL514171 AL514171

ALIGNMENTS

RESULT 1
CB400039/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

87 bp mRNA linear EST 15-MAY-2003
OSTF167D8_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB400039
CB400039.1 GI:30741766
EST.

Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 87)

Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
, C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
, J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P.,
Pracek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.

C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press

JOURNAL
COMMENT

Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180

Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES

Location/Qualifiers

1. .87

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

26 a 16 c 21 g 24 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 87;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 CAGCTTCTCTGTACAAAGTTGG 25

Db

27 CAGCTTCTCTGTACAAAGTTGG 6

RESULT 2

CB392047/c

LOCUS

CB392047 90 bp mRNA linear EST 15-MAY-2003

OSTF163A10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION

CB392047.1 GI:30733757

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 90)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@dfci.harvard.edu or

marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES

Location/Qualifiers

1. .90

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

27 a 18 c 17 g 28 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 90;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 CAGCTTCTCTGTACAAAGTTGG 25

Db

31 CAGCTTCTCTGTACAAAGTTGG 10

RESULT 3

CB402537/c

LOCUS

CB402537 92 bp mRNA linear EST 15-MAY-2003

OSTF214C1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION

CB402537

VERSION

CB402537.1 GI:30744264

KEYWORDS

EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 92)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@dfci.harvard.edu or

marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES

Location/Qualifiers

1. .92

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

25 a 13 c 26 g 28 t

ORIGIN

LOCUS	CB400591	95 bp	mRNA	linear	EST 15-MAY-2003			
DEFINITION	OSTF179E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.							
ACCESSION	CB400591							
VERSION	CB400591.1	GI:30742318						
KEYWORDS	EST.							
SOURCE	Caenorhabditis elegans							
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.							
REFERENCE	1 (bases 1 to 95)							
AUTHORS	Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevret, E., Papasotiropoulos, V., Tolias, P.P., Placet, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.							
TITLE	C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression							
JOURNAL	Nat. Genet., (2003) In press							
COMMENT	Contact: Vidal M Marc Vidal Laboratory Dana Farber Cancer Institute 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA Tel: 617 632 5180 Fax: 617 632 5739 Email: Marc.Vidal@dfci.harvard.edu Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david.hill@dfci.harvard.edu or marc.vidal@dfci.harvard.edu POLYA=NO.							
FEATURES	Location/Qualifiers							
source	1..95							
	/organism="Caenorhabditis elegans"							
	/mol_type="mRNA"							
	/strain="N2"							
	/db_xref="taxon:6239"							
	/sex="Hermaphrodite and male"							
	/tissue_type="whole animal"							
	/dev_stage="mixed stage"							
	/clone_lib="AD-wrmcDNA"							
	/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"							
BASE COUNT	39 a	16 c	16 g	24 t				
ORIGIN								
Query Match	88.0%; Score 22; DB 14; Length 95;							
Best Local Similarity	100.0%; Pred. No. 24;							
Matches	22; Conservative	0; Mismatches	0; Indels	0; Gaps	0; Gaps			
Qy	4	CAGCTTCTTGTACAAAGTTGG	25					
Db	29	CAGCTTCTTGTACAAAGTTGG	8					
RESULT 6								
CB401751/c								
LOCUS	CB401751	95 bp	mRNA	linear	EST 15-MAY-2003			
DEFINITION	OSTF198G7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.							
ACCESSION	CB401751							
VERSION	CB401751.1	GI:30743478						
KEYWORDS	EST.							
SOURCE	Caenorhabditis elegans							
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.							
REFERENCE	1 (bases 1 to 95)							
AUTHORS	Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson							

J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

FEATURES

Location/Qualifiers

1..97

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

28 a 20 c 19 g 28 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 22; DB 14; Length 95;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 CAGCTTTCTTGTCACAAAGTTGG 25

DB

29 CAGCTTTCTTGTCACAAAGTTGG 8

RESULT 7

CB401179/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

COMMENT

1 (bases 1 to 97)

Rhabditidae; Peloderinae; Caenorhabditis.

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLYA-No.

FEATURES

Location/Qualifiers

1..97

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

30 a 17 c 16 g 34 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 22; DB 14; Length 97;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 CAGCTTTCTTGTCACAAAGTTGG 25

DB

32 CAGCTTTCTTGTCACAAAGTTGG 11

RESULT 8

CB402581/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

COMMENT

1 (bases 1 to 98)

Rhabditidae; Peloderinae; Caenorhabditis.

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@dfci.harvard.edu or

marc_vidal@dfci.harvard.edu

POLYA-No.

FEATURES

Location/Qualifiers

1..98

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

```

/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
24 a 22 c 20 g 32 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 32 CAGCTTCTTGTACAAAGTTGG 11

RESULT 9
CB392051/c
LOCUS 100 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF163A3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB392051
VERSION CB392051.1 GI:30733761
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 100)
AUTHORS Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevret, E., Papanastasiopoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu
POLYA-No. Location/Qualifiers
1. .100
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
32 a 24 c 18 g 26 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 30 CAGCTTCTTGTACAAAGTTGG 9

RESULT 11

```

```

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 32 CAGCTTCTTGTACAAAGTTGG 11

RESULT 10
CB400512/c
LOCUS 100 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF17G3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB400512
VERSION CB400512.1 GI:30742239
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 100)
AUTHORS Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevret, E., Papanastasiopoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu
POLYA-No. Location/Qualifiers
1. .100
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
31 a 22 c 14 g 33 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db 30 CAGCTTCTTGTACAAAGTTGG 9

RESULT 11

```

CB392040/C
 LOCUS CB392040 102 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF162H10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB392040
 VERSION CB392040.1 GI:30733750
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 102)
 AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression
 JOURNAL Nat. Genet., (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
 POLYA=No.
 FEATURES Location/Qualifiers
 source 1..102
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pC86"
 BASE COUNT 31 a 14 c 22 g 35 t
 ORIGIN
 Query Match 88.0%; Score 22; DB 14; Length 102;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CAGCTTCTCTGTACAAAGTTGG 25
 |||||
 Db 35 CAGCTTCTCTGTACAAAGTTGG 14
 |||||
 RESULT 12
 LOCUS CB401874/C
 DEFINITION OSTF202B11_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB401874
 VERSION CB401874.1 GI:30743601
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 103)
 AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression
 JOURNAL Nat. Genet., (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
 POLYA=No.
 FEATURES Location/Qualifiers
 source 1..103
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC96"
 BASE COUNT 21 a 18 c 21 g 43 t
 ORIGIN
 Query Match 88.0%; Score 22; DB 14; Length 103;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CAGCTTCTCTGTACAAAGTTGG 25
 |||||
 Db 36 CAGCTTCTCTGTACAAAGTTGG 15
 |||||
 RESULT 13
 LOCUS CB388456/C
 DEFINITION OSTF099E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB388456
 VERSION CB388456.1 GI:30730166
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 107)
 AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression
 JOURNAL Nat. Genet., (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA-No.

Location/Qualifiers

1. .117

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/notes="The AD-wrmcDNA library was generated with poly(A) +

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

34 a 18 c 16 g 39 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 107;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25

|||||

Db 29 CAGCTTCTTGTACAAAGTTGG 8

RESULT 14

CB394444

LOCUS

DEFINITION OSTR137H4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB394444

VERSION CB394444.1

KEYWORDS EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 111)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet. (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA-No.

Location/Qualifiers

1. .111

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A) +

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

32 a 18 c 22 g 39 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 111;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25

|||||

Db 71 CAGCTTCTTGTACAAAGTTGG 92

RESULT 15

CB402012/c

LOCUS

DEFINITION OSTRF205B3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB402012

VERSION CB402012.1

KEYWORDS EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 114)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet. (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA-No.

Location/Qualifiers

1. .114

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A) +

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

```

BASE COUNT      32 a      27 c      26 g      29 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
    |||||
Db 34 CAGCTTTCTTGTACAAAGTTGG 13

RESULT 16
CB392055/c
LOCUS
DEFINITION OSTF163B1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
ACCESSION CB392055
VERSION CB392055.1 GI:30733765
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
TITLE
JOURNAL
COMMENT
FEATURES
    source
    1..120
    /organism="Caenorhabditis elegans"
    /mol_type="mRNA"
    /strain="N2"
    /db_xref="taxon:6239"
    /sex="Hermaphrodite and male"
    /tissue_type="whole animal"
    /dev_stage="mixed stage"
    /clone_lib="AD-wrmcDNA"
    /note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
BASE COUNT      36 a      27 c      22 g      35 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
    |||||
Db 56 CAGCTTTCTTGTACAAAGTTGG 35

RESULT 17
CB400382/c
LOCUS
DEFINITION OSTF175B7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
ACCESSION CB400382
VERSION CB400382.1 GI:30742109
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
TITLE
JOURNAL
COMMENT
FEATURES
    source
    1..120
    /organism="Caenorhabditis elegans"
    /mol_type="mRNA"
    /strain="N2"
    /db_xref="taxon:6239"
    /sex="Hermaphrodite and male"
    /tissue_type="whole animal"
    /dev_stage="mixed stage"
    /clone_lib="AD-wrmcDNA"
    /note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
BASE COUNT      42 a      22 c      19 g      37 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
    |||||
Db 61 CAGCTTTCTTGTACAAAGTTGG 40

RESULT 18
CB399813/c
LOCUS
DEFINITION OSTF163C2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
ACCESSION CB399813
VERSION CB399813.1 GI:30741540
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
TITLE
JOURNAL
COMMENT
FEATURES
    source
    1..120
    /organism="Caenorhabditis elegans"
    /mol_type="mRNA"
    /strain="N2"
    /db_xref="taxon:6239"
    /sex="Hermaphrodite and male"
    /tissue_type="whole animal"
    /dev_stage="mixed stage"
    /clone_lib="AD-wrmcDNA"
    /note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
BASE COUNT      42 a      22 c      19 g      37 t
ORIGIN
Query Match      88.0%; Score 22; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
    |||||
Db 61 CAGCTTTCTTGTACAAAGTTGG 40

```

AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

JOURNAL Nat. Genet., (2003) In press
COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES Location/Qualifiers
 1..124
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 36 a 31 c 22 g 35 t
ORIGIN
 Query Match 88.0%; Score 22; DB 14; Length 124;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CAGCTTCTTGTACAAAGTTGG 25
 Db 61 CAGCTTCTTGTACAAAGTTGG 40

RESULT 19
CB400130/c
LOCUS CB400130 126 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF169C5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB400130
VERSION CB400130.1 GI:30741857
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 126)
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet., (2003) In press
COMMENT Contact: Vidal M
 Marc Vidal Laboratory

Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES Location/Qualifiers
 1..126
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 38 a 27 c 23 g 38 t
ORIGIN
 Query Match 88.0%; Score 22; DB 14; Length 126;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CAGCTTCTTGTACAAAGTTGG 25
 Db 61 CAGCTTCTTGTACAAAGTTGG 40

RESULT 20
CB400226/c
LOCUS CB400226 128 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF171D4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB400226
VERSION CB400226.1 GI:30741953
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 128)
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet., (2003) In press
COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES Location/Qualifiers
 1..128
 source

```

/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
41 a 27 c 22 g 38 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 61 CAGCTTTCTTGTACAAAGTTGG 40
|||||

RESULT 21
LOCUS CB401894 128 bp mRNA linear EST 15-MAY-2003
DEFINITION OSF202C5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB401894
VERSION CB401894.1 GI:30743611
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 128)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
COMMENT Contact: Vidal M
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..128
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
41 a 27 c 22 g 38 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 61 CAGCTTTCTTGTACAAAGTTGG 40
|||||

RESULT 21
LOCUS CB401894 128 bp mRNA linear EST 15-MAY-2003
DEFINITION OSF202C5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB401894
VERSION CB401894.1 GI:30743611
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 128)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
COMMENT Contact: Vidal M
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..128
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
41 a 27 c 22 g 38 t
BASE COUNT
ORIGIN

```

```

BASE COUNT 32 a 23 c 23 g 50 t
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 60 CAGCTTTCTTGTACAAAGTTGG 39
|||||

RESULT 22
LOCUS CB401218 129 bp mRNA linear EST 15-MAY-2003
DEFINITION OSF191C6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB401218
VERSION CB401218.1 GI:30742945
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 129)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
COMMENT Contact: Vidal M
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..129
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
37 a 28 c 20 g 44 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 129;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 62 CAGCTTTCTTGTACAAAGTTGG 41
|||||

```

```

RESULT 23
CB398923
LOCUS
DEFINITION 227 bp mRNA linear EST 15-MAY-2003
CB398923_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB398923
VERSION
CB398923.1 GI:30740650
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
REFERENCE
1 (bases 1 to 227)
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.I., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david.hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.
FEATURES
Location/Qualifiers
1..227
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 72 a 47 c 42 g 66 t
ORIGIN
Query Match 88.0%; Score 22; DB 14; Length 227;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
|||||
Db 108 CAGCTTCTCTGTACAAAGTTGG 129

RESULT 24
CB401020/c
LOCUS
DEFINITION 247 bp mRNA linear EST 15-MAY-2003
CB401020_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB401020
VERSION
CB401020.1 GI:30742747
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
REFERENCE
1 (bases 1 to 247)
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.I., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david.hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.
FEATURES
Location/Qualifiers
1..247
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 72 a 44 c 47 g 84 t
ORIGIN
Query Match 88.0%; Score 22; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
|||||
Db 75 CAGCTTCTCTGTACAAAGTTGG 54

RESULT 25
CB395877
LOCUS
DEFINITION 262 bp mRNA linear EST 15-MAY-2003
CB395877_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB395877
VERSION
CB395877.1 GI:30737588
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
REFERENCE
1 (bases 1 to 262)
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.I., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M

```

```

REFERENCE
AUTHORS
1 (bases 1 to 247)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.I., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david.hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.
FEATURES
Location/Qualifiers
1..247
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 72 a 44 c 47 g 84 t
ORIGIN
Query Match 88.0%; Score 22; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
|||||
Db 75 CAGCTTCTCTGTACAAAGTTGG 54

RESULT 25
CB395877
LOCUS
DEFINITION 262 bp mRNA linear EST 15-MAY-2003
CB395877_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB395877
VERSION
CB395877.1 GI:30737588
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
REFERENCE
1 (bases 1 to 262)
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.I., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Toliaas,P.P.,
Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M

```


Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617-632 5180
 Fax: 617 632 5739
 Email: Marc_Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES

source Location/Qualifiers

1..262
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
 77 a 54 c 48 g 83 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 262;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTCTGACAAAGTTGG 25

Db 128 CAGCTTCTTCTGACAAAGTTGG 149

RESULT 26

CB395890

LOCUS

CB395890_1 AD-wrmcDNA Caenorhabditis elegans cDNA, linear EST 15-MAY-2003

DEFINITION

CB395890

ACCESSION

CB395890.1

VERSION

CB395890.1

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

REFERENCE

AUTHORS

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P., Placsek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE

C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

JOURNAL

CONTACT

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc_Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLYA=No.

Location/Qualifiers

source

1..263

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

78 a 51 c 54 g 80 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 263;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTCTGACAAAGTTGG 25

Db 132 CAGCTTCTTCTGACAAAGTTGG 153

RESULT 27

LOCUS

B1174869

DEFINITION

OSTF061D8_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to

K04A8.3, mRNA sequence.

ACCESSION

B1174869

VERSION

B1174869.1

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

REFERENCE

AUTHORS

Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitt, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F., Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.

TITLE

Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans

JOURNAL

MEDLINE

21135099

PUBMED

11242119

COMMENT

Contact: Reboul J, Vaglio P

Marc Vidal Laboratory

Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 2425

Email: Jerome.Reboul@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact Jerome.Reboul@dfci.harvard.edu or philippe.vaglio@dfci.harvard.edu

POLYA=No.

Location/Qualifiers

1..380

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the

Location/Qualifiers

subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

```

BASE COUNT      112 a   65 c   106 g   97 t
ORIGIN
Query Match      88.0%; Score 22; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db  333 CAGCTTCTTGTACAAAGTTGG 354

RESULT 28
BI174871
LOCUS
DEFINITION      435 bp mRNA linear EST 09-JUL-2001
OSTF061810.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
ACCESSION      BI174871
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-I, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
21135099
11242119
PUBMED
COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact Jerome.Reboul@dfci.harvard.edu or
philippe.vaglio@dfci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..435
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT      142 a   78 c   86 g   129 t
ORIGIN
Query Match      88.0%; Score 22; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db  393 CAGCTTCTTGTACAAAGTTGG 414

RESULT 29
BI174883
LOCUS
DEFINITION      460 bp mRNA linear EST 09-JUL-2001
OSTF061810.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
ACCESSION      BI174883
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-I, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
21135099
11242119
PUBMED
COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact Jerome.Reboul@dfci.harvard.edu or
philippe.vaglio@dfci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..460
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT      121 a   100 c   122 g   117 t
ORIGIN
Query Match      88.0%; Score 22; DB 12; Length 460;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db  397 CAGCTTCTTGTACAAAGTTGG 418

RESULT 30
BI174361
LOCUS
DEFINITION      467 bp mRNA linear EST 09-JUL-2001
OSTF042E6.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
ACCESSION      BI174361
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-I, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
21135099
11242119
PUBMED
COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact Jerome.Reboul@dfci.harvard.edu or
philippe.vaglio@dfci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..467
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT      142 a   78 c   86 g   129 t
ORIGIN
Query Match      88.0%; Score 22; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 CAGCTTCTTGTACAAAGTTGG 25
|||||
Db  393 CAGCTTCTTGTACAAAGTTGG 414

```

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 467)

REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,
Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

JOURNAL
MEDLINE
PUBMED
11242119

COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact Jerome.reboul@fci.harvard.edu or
philippe.vaglio@fci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..467
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT
ORIGIN
153 a 87 c 101 g 126 t

Query Match 88.0%; Score 22; DB 12; Length 467;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||

Db 439 CAGCTTCTTGTACAAAGTTGG 460
|||||

RESULT 31
BII74878
LOCUS
DEFINITION
OSTP061F11.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
W02D7.3, mRNA sequence.
ACCESSION
BII74878
VERSION
BII74878.1 GI:14640681
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,
Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

JOURNAL
MEDLINE
PUBMED
11242119

Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact Jerome.reboul@fci.harvard.edu or
philippe.vaglio@fci.harvard.edu
POLYA=No.

FEATURES
source
Location/Qualifiers
1..480
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT
ORIGIN
140 a 124 c 80 g 136 t

Query Match 88.0%; Score 22; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
|||||

Db 408 CAGCTTCTTGTACAAAGTTGG 429
|||||

RESULT 32
BII74375
LOCUS
DEFINITION
OSTP042G8.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
B0280.4, mRNA sequence.
ACCESSION
BII74375
VERSION
BII74375.1 GI:14640178
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,
Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

JOURNAL
MEDLINE
PUBMED
11242119

COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact Jerome.reboul@fci.harvard.edu or
philippe.vaglio@fci.harvard.edu
POLYA=No.

```

FEATURES
  source
    Location/Qualifiers
      1. .501
        /organism="Caenorhabditis elegans"
        /mol_type="mRNA"
        /strain="N2"
        /db_xref="taxon:6239"
        /sex="Hermaphrodite and male"
        /tissue_type="whole animal"
        /dev_stage="mixed stage"
        /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
      BASE COUNT 168 a 104 c 93 g 136 t
      ORIGIN
        Query Match 88.0%; Score 22; DB 12; Length 501;
        Best Local Similarity 100.0%; Pred. No. 40;
        Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      QY 4 CAGCTTTCTTGTACAAAGTTGG 25
        |||||||
      Db 453 CAGCTTTCTTGTACAAAGTTGG 474

      RESULT 33
      BI174868
      LOCUS
      DEFINITION
        B1174868 508 bp mRNA linear EST 09-JUL-2001
        OSTF061D7.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
        F28A10.3, mRNA sequence.
      ACCESSION
        BI174868
      VERSION
        BI174868.1 GI:14640671
      KEYWORDS
        EST.
      SOURCE
        Caenorhabditis elegans
        ORGANISM
        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
        ; Rhabditidae; Pelodierinae; Caenorhabditis.
      REFERENCE
        1 (bases 1 to 508)
      AUTHORS
        Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
        Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
        Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
        Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
      TITLE
        Open-reading-frame sequence tags (OSTs) support the existence of at
        least 17,300 genes in C. elegans
      JOURNAL
        Nat. Genet. 27 (3), 332-336 (2001)
      MEDLINE
        21135099
      PUBMED
        11242119
      COMMENT
        Contact: Reboul J, Vaglio P
        Marc Vidal Laboratory
        Dana Farber Cancer Institute
        44 Binney Street, Boston, MA 02115, USA
        Tel: 617 632 5180
        Fax: 617 632 2425
        Email: Jerome.Reboul@dfci.harvard.edu
        Sequence tag of Gateway entry clones. The primers used were
        designed on the predicted protein encoding ORF. C. elegans ORFeome
        cloning project : Contact jerome_reboul@dfci.harvard.edu or
        philippe_vaglio@dfci.harvard.edu
        POLYA=No.
      FEATURES
        Location/Qualifiers
          1. .508
            /organism="Caenorhabditis elegans"
            /mol_type="mRNA"
            /strain="N2"
            /db_xref="taxon:6239"
            /sex="Hermaphrodite and male"
            /tissue_type="whole animal"
            /dev_stage="mixed stage"
            /clone_lib="AD-wrmcDNA"
            /note="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"
          BASE COUNT 169 a 134 c 119 g 127 t
          ORIGIN
            Query Match 88.0%; Score 22; DB 12; Length 549;
            Best Local Similarity 100.0%; Pred. No. 42;
            Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

            QY 4 CAGCTTTCTTGTACAAAGTTGG 25
              |||||||

```

```

all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
      BASE COUNT 121 a 102 c 105 g 180 t
      ORIGIN
        Query Match 88.0%; Score 22; DB 12; Length 508;
        Best Local Similarity 100.0%; Pred. No. 41;
        Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      QY 4 CAGCTTTCTTGTACAAAGTTGG 25
        |||||||
      Db 436 CAGCTTTCTTGTACAAAGTTGG 457

      RESULT 34
      BI174892
      LOCUS
      DEFINITION
        B1174892 549 bp mRNA linear EST 09-JUL-2001
        OSTF061G9.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
        P32D1.6, mRNA sequence.
      ACCESSION
        BI174892
      VERSION
        BI174892.1 GI:14640695
      KEYWORDS
        EST.
      SOURCE
        Caenorhabditis elegans
        ORGANISM
        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
        ; Rhabditidae; Pelodierinae; Caenorhabditis.
      REFERENCE
        1 (bases 1 to 549)
      AUTHORS
        Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
        Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
        Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
        Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
      TITLE
        Open-reading-frame sequence tags (OSTs) support the existence of at
        least 17,300 genes in C. elegans
      JOURNAL
        Nat. Genet. 27 (3), 332-336 (2001)
      MEDLINE
        21135099
      PUBMED
        11242119
      COMMENT
        Contact: Reboul J, Vaglio P
        Marc Vidal Laboratory
        Dana Farber Cancer Institute
        44 Binney Street, Boston, MA 02115, USA
        Tel: 617 632 5180
        Fax: 617 632 2425
        Email: Jerome.Reboul@dfci.harvard.edu
        Sequence tag of Gateway entry clones. The primers used were
        designed on the predicted protein encoding ORF. C. elegans ORFeome
        cloning project : Contact jerome_reboul@dfci.harvard.edu or
        philippe_vaglio@dfci.harvard.edu
        POLYA=No.
      FEATURES
        Location/Qualifiers
          1. .549
            /organism="Caenorhabditis elegans"
            /mol_type="mRNA"
            /strain="N2"
            /db_xref="taxon:6239"
            /sex="Hermaphrodite and male"
            /tissue_type="whole animal"
            /dev_stage="mixed stage"
            /clone_lib="AD-wrmcDNA"
            /note="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"
          BASE COUNT 169 a 134 c 119 g 127 t
          ORIGIN
            Query Match 88.0%; Score 22; DB 12; Length 549;
            Best Local Similarity 100.0%; Pred. No. 42;
            Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

            QY 4 CAGCTTTCTTGTACAAAGTTGG 25
              |||||||

```

5

11242119
 PUBMED
 COMMENT
 Contact: Reboul J, Vaglio P
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 44 Binney Street, Boston, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 2425
 Email: Jerome.Reboul@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact jerome_reboul@dfci.harvard.edu or
 philippe_vaglio@dfci.harvard.edu
 POLYA=No.

FEATURES

source

Location/Qualifiers
 1. .613
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"

/db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="RD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

BASE COUNT 199 a 143 c 121 g 150 t
 ORIGIN
 Query Match 88.0%; Score 22; DB 12; Length 613;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAAAGTTGG 25
 |||||||
 Db 551 CAGCTTCTTGTACAAAGTTGG 572

RESULT 38

CB960041/c

LOCUS

DEFINITION CB960041 1388 bp mRNA linear EST 29-APR-2003
 IMAGE:30340779 5', mRNA sequence.

ACCESSION

CB960041

VERSION

CB960041.1 GI:30216157

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1388)

NIH-MGC http://mgs.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hanson
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM371 row: d column: 04
 High quality sequence start: 138
 High quality sequence stop: 355.

FEATURES

source

1. .1388

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:30340779"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_147"

/note="Organ: placenta; Vector: pBluescriptR; Site:1:
 all-XhoI; Site 2: BamH; Oligo-dr primed using primer
 5'-TTTTTTTTTTTTTNN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH MGC library."

BASE COUNT 429 a 271 c 314 g 361 t 13 others
 ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 1388;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAAAGTTGG 25

|||||

Db 154 CAGCTTCTTGTACAAAGTTGG 133

RESULT 39

AL515389/c

LOCUS

DEFINITION

AL515389 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone

ACCESSION

AL515389

VERSION

AL515389.2 GI:30465271

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 559)

Li W.B., Gruber C., Jesse J. and Polayes D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

COMMENT

On Feb 13, 2001 this sequence version replaced gi:12778882.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1606.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CL0BB0192B04FP1&cluster=1606.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CL0BB0192B04FP1.
 Location/Qualifiers

1. .559

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CL0BB0192B04"

/tissue_type="NEUROBLASTOMA"

/clone_lib="Homo sapiens NEUROBLASTOMA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

BASE COUNT 190 a 78 c 68 g 163 t

ORIGIN

Query Match 84.0%; Score 21; DB 9; Length 559;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTCACAAAGTTG 24
 |||||
 Db 40 CAGCTTCTTGTCACAAAGTTG 20

RESULT 40
 CD048261 982 bp mRNA linear EST 09-MAY-2003
 LOCUS AGENCOURT_13971692 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.
 CD048261
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 982)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 CDNA Library Preparation: Gina Zastrow-Hayes
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: NDKM41 row: p column: 19
 High quality sequence start: 11
 High quality sequence stop: 472.
 Location/Qualifiers

FEATURES
 source
 1..982
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 172"
 /notes="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
 LIBR_PRIMING - oligo dt; METHOD - full-length enriched;
 Embryonic Stem Cells HI; LIBR PROVIDER - Bradfield"
 BASE COUNT 203 a 198 c 219 g 146 t 216 others
 ORIGIN

Query Match 84.0%; Score 21; DB 14; Length 982;
 Best Local Similarity 95.5%; Pred. No. 1.4e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTCACAAAGTTG 25
 |||||
 Db 590 CAGCTTCTTGTCACAAAGTTG 611

Search completed: November 7, 2003, 00:21:01
 Job time : 1094.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:12:53 ; Search time 28 Seconds
(without alignments)
394.092 Million cell updates/sec

Title: US-10-055-001A-10

Perfect score: 25
Sequence: 1 gtccagctttttgtcaaaagtgg 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3	US-09-233-493-15
2	25	100.0	25	3	US-09-005-476-15
3	25	100.0	25	3	US-09-233-492-15
4	25	100.0	25	3	US-09-296-280-15
5	25	100.0	25	4	US-09-498-074-15
6	25	100.0	25	5	PCT-US96-10082A-15
7	23.8	95.2	25	3	US-09-296-280-43
8	23.4	93.6	25	3	US-09-233-493-11
9	23.4	93.6	25	3	US-09-233-493-16
10	23.4	93.6	25	3	US-09-005-476-11
11	23.4	93.6	25	3	US-09-005-476-16
12	23.4	93.6	25	3	US-09-233-492-11
13	23.4	93.6	25	3	US-09-233-492-16
14	23.4	93.6	25	3	US-09-296-280-16
15	23.4	93.6	25	4	US-09-498-074-11
16	23.4	93.6	25	4	US-09-498-074-16
17	23.4	93.6	25	5	PCT-US96-10082A-11
18	23.4	93.6	25	5	PCT-US96-10082A-16
19	22.4	89.6	25	3	US-09-233-493-9
20	22.4	89.6	25	3	US-09-005-476-9
21	22.4	89.6	25	3	US-09-233-492-9
22	22.4	89.6	25	3	US-09-296-280-9
23	22.4	89.6	25	4	US-09-498-074-9
24	22.4	89.6	25	5	PCT-US96-10082A-9
25	22	88.0	25	3	US-09-296-280-42
26	21.8	87.2	201	1	US-08-021-667A-18
27	21.8	87.2	201	1	US-08-410-544-18

28	21.8	87.2	201	1	US-08-728-785A-18
29	21.8	87.2	4909	3	US-08-556-978B-78
30	21.8	87.2	7652	1	US-07-590-988A-1
31	20.8	83.2	25	3	US-09-233-493-10
32	20.8	83.2	25	3	US-09-005-476-10
33	20.8	83.2	25	3	US-09-233-492-10
34	20.8	83.2	25	3	US-09-296-280-10
35	20.8	83.2	25	3	US-09-296-280-11
36	20.8	83.2	25	4	US-09-498-074-10
37	20.8	83.2	25	5	PCT-US96-10082A-10
38	20.4	81.6	25	3	US-09-233-493-5
39	20.4	81.6	25	3	US-09-233-493-12
40	20.4	81.6	25	3	US-09-233-493-14
41	20.4	81.6	25	3	US-09-005-476-5
42	20.4	81.6	25	3	US-09-005-476-12
43	20.4	81.6	25	3	US-09-005-476-14
44	20.4	81.6	25	3	US-09-233-492-5
45	20.4	81.6	25	3	US-09-233-492-12

ALIGNMENTS

RESULT 1
US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-15


```
Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 2
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-15

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 3
US-09-233-492-15
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 4
US-09-296-280-15
; Sequence 15, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-296-280-15

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 5

US-09-498-074-15
; Sequence 15, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-15

Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 6

PCT-US96-10082A-15
; Sequence 15, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America

; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
PCT-US96-10082A-15

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 7

US-09-296-280-43
; Sequence 43, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-43

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.24;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|:|:|:|:|:|
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 8

US-09-233-493-11
; Sequence 11, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-11

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|:|:|:|:|:|
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 9

US-09-233-493-16
; Sequence 16, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered

; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-16

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|:|:~|:~|:~|:~|:~|
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 10

US-09-005-476-11
; Sequence 11, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-11

Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 12
US-09-233-492-11
; Sequence 11, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-11

Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 13
US-09-233-492-16
; Sequence 16, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-16

Query Match          93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-16
;
; Query Match 93.6%; Score 23.4; DB 3; Length 25;
; Best Local Similarity 96.0%; Pred. No. 0.34;
; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 15
US-09-498-074-11
; Sequence 11, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-11
;
; Query Match 93.6%; Score 23.4; DB 4; Length 25;
; Best Local Similarity 96.0%; Pred. No. 0.34;
; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 16
US-09-498-074-16
; Sequence 16, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-296-280-16
;
; Query Match 93.6%; Score 23.4; DB 3; Length 25;
; Best Local Similarity 96.0%; Pred. No. 0.34;

```

```

; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-16

Query Match 93.6%; Score 23.4; DB 4; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 17
PCT-US96-10082A-11
; Sequence 11, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-11

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 18
PCT-US96-10082A-16
; Sequence 16, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-16

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-11

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 18
PCT-US96-10082A-16
; Sequence 16, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-16

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

Db 1 GTTCAGCTTTCTGTACAAAGTTG 25

RESULT 19

US-09-233-493-9
; Sequence 9, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 05/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-9
Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAAGTTG 24

RESULT 20

US-09-005-476-9
; Sequence 9, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-005-476-9

Query Match

89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.88;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTACAAAGTTG 24

Db 1 GTTCAGCTTTCTGTACAAAGTTG 24

RESULT 21

US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995

```
;
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-9
;
; Query Match 89.6%; Score 22.4; DB 3; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.88;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
; |||||
; Db 1 GTTCAGCTTTTGTACAAAGTTG 24
;
; RESULT 22
; US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; US-09-296-280-9
;
; Query Match 89.6%; Score 22.4; DB 3; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.88;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
; |||||
; Db 1 GTTCAGCTTTTGTACAAAGTTG 24
;
; RESULT 23
; US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
;
; Query Match 89.6%; Score 22.4; DB 3; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.88;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
; |||||
; Db 1 GTTCAGCTTTTGTACAAAGTTG 24
;
; RESULT 24
; PCT-US96-10082A-9
; Sequence 9, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
```

```
;
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-9
;
; Query Match 89.6%; Score 22.4; DB 4; Length 25;
; Best Local Similarity 95.8%; Pred. No. 0.88;
; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
; |||||
; Db 1 GTTCAGCTTTTGTACAAAGTTG 24
;
; RESULT 24
; PCT-US96-10082A-9
; Sequence 9, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
```


CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
PCT-US96-10082A-9

Query Match 89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.88;
Matches 23; Conservative 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 25
US-09-296-280-42

Sequence 42, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-42

Query Match 88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 26
US-08-021-667A-18

Sequence 18, Application US/08021667A
Patent No. 5434049
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus

STREET: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021.667A
FILING DATE: 19930224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-828-0300
TELEFAX: 202-828-0380
TELEX: 440280/248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-021-667A-18

Query Match 87.2%; Score 21.8; DB 1; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 25
|||||
DB 40 GTTCAGCTTTTGTACAAAGTTG 64

RESULT 27

US-08-410-544-18
Sequence 18, Application US/08410544
Patent No. 5607646
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410.544
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:

NAME	Terry, David T.	NAME	Terry, David T.
REGISTRATION NUMBER:	20,178	REGISTRATION NUMBER:	20,178
REFERENCE/DOCKET NUMBER:	520.31930X00	REFERENCE/DOCKET NUMBER:	520.31930X00
TELEPHONE:	202-828-0300	TELEPHONE:	202-828-0300
TELEFAX:	202-828-0380	TELEFAX:	202-828-0380
TELEX:	248545	TELEX:	248545
INFORMATION FOR SEQ ID NO:	18:	INFORMATION FOR SEQ ID NO:	18:
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH:	201 base pairs	LENGTH:	201 base pairs
TYPE:	nucleic acid	TYPE:	nucleic acid
STRANDEDNESS:	single	STRANDEDNESS:	single
TOPOLOGY:	linear	TOPOLOGY:	linear
MOLECULE TYPE:	DNA (genomic)	MOLECULE TYPE:	DNA (genomic)
HYPOTHETICAL:	YES	HYPOTHETICAL:	YES
ANTI-SENSE:	NO	ANTI-SENSE:	NO
US-08-410-544-18		US-08-410-544-18	
Query Match	87.2%; Score 21.8; DB 1; Length 201;	Query Match	87.2%; Score 21.8; DB 1; Length 201;
Best Local Similarity	92.0%; Pred. No. 1.7;	Best Local Similarity	92.0%; Pred. No. 1.7;
Mismatches	23; Conservative 0; Indels 0; Gaps 0;	Mismatches	23; Conservative 0; Indels 0; Gaps 0;
QY	1 GTTCAGCTTTTGTACAAAGTTGG 25	QY	1 GTTCAGCTTTTGTACAAAGTTGG 25
Db	40 GTTCAGCTTTTGTACAAAGTTGG 64	Db	40 GTTCAGCTTTTGTACAAAGTTGG 64
RESULT 28		RESULT 28	
US-08-728-785A-18		US-08-728-785A-18	
Sequence 18, Application US/08728785A		Sequence 18, Application US/08728785A	
Patent No. 5817506		Patent No. 5817506	
GENERAL INFORMATION:		GENERAL INFORMATION:	
APPLICANT:	Okano, Kazunori	APPLICANT:	Okano, Kazunori
TITLE OF INVENTION:	POLYNUCLEOTIDE CAPTURING TIP AND	TITLE OF INVENTION:	POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION:	POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION	TITLE OF INVENTION:	POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION:	METHOD USING SAME	TITLE OF INVENTION:	METHOD USING SAME
NUMBER OF SEQUENCES:	18	NUMBER OF SEQUENCES:	18
CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Antonelli, Terry, Stout & Kraus	ADDRESSEE:	Antonelli, Terry, Stout & Kraus
STREET:	Suite 1800, 1300 No. 5817506th Seventeenth St.	STREET:	Suite 1800, 1300 No. 5817506th Seventeenth St.
CITY:	Arlington	CITY:	Arlington
STATE:	VA	STATE:	VA
COUNTRY:	USA	COUNTRY:	USA
ZIP:	22209	ZIP:	22209
COMPUTER READABLE FORM:		COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk	MEDIUM TYPE:	Floppy disk
OPERATING SYSTEM:	PC-DOS/MS-DOS	OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.25	SOFTWARE:	PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER:	US/08/728,785A	APPLICATION NUMBER:	US/08/728,785A
FILING DATE:	10-OCT-1996	FILING DATE:	10-OCT-1996
CLASSIFICATION:	435	CLASSIFICATION:	435
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/410,544	APPLICATION NUMBER:	08/410,544
FILING DATE:	21-MAR-1995	FILING DATE:	21-MAR-1995
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/021,667	APPLICATION NUMBER:	08/021,667
FILING DATE:	24-FEB-1993	FILING DATE:	24-FEB-1993
ATTORNEY/AGENT INFORMATION:		ATTORNEY/AGENT INFORMATION:	
NAME:	Terry, David T.	NAME:	Terry, David T.
REGISTRATION NUMBER:	20,178	REGISTRATION NUMBER:	20,178
REFERENCE/DOCKET NUMBER:	520.31930X00	REFERENCE/DOCKET NUMBER:	520.31930X00
TELEPHONE:	703-312-6600	TELEPHONE:	703-312-6600
TELEFAX:	703-312-6666	TELEFAX:	703-312-6666
INFORMATION FOR SEQ ID NO:	18:	INFORMATION FOR SEQ ID NO:	18:
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH:	201 base pairs	LENGTH:	201 base pairs
TYPE:	nucleic acid	TYPE:	nucleic acid
STRANDEDNESS:	single	STRANDEDNESS:	single
TOPOLOGY:	linear	TOPOLOGY:	linear

NAME	Terry, David T.	NAME	Terry, David T.
REGISTRATION NUMBER:	20,178	REGISTRATION NUMBER:	20,178
REFERENCE/DOCKET NUMBER:	520.31930X00	REFERENCE/DOCKET NUMBER:	520.31930X00
TELEPHONE:	202-828-0300	TELEPHONE:	202-828-0300
TELEFAX:	202-828-0380	TELEFAX:	202-828-0380
TELEX:	248545	TELEX:	248545
INFORMATION FOR SEQ ID NO:	18:	INFORMATION FOR SEQ ID NO:	18:
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH:	201 base pairs	LENGTH:	201 base pairs
TYPE:	nucleic acid	TYPE:	nucleic acid
STRANDEDNESS:	single	STRANDEDNESS:	single
TOPOLOGY:	linear	TOPOLOGY:	linear
MOLECULE TYPE:	DNA (genomic)	MOLECULE TYPE:	DNA (genomic)
HYPOTHETICAL:	YES	HYPOTHETICAL:	YES
ANTI-SENSE:	NO	ANTI-SENSE:	NO
US-08-410-544-18		US-08-410-544-18	
Query Match	87.2%; Score 21.8; DB 1; Length 201;	Query Match	87.2%; Score 21.8; DB 1; Length 201;
Best Local Similarity	92.0%; Pred. No. 1.7;	Best Local Similarity	92.0%; Pred. No. 1.7;
Matches	23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches	23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 GTTCAGCTTTTGTACAAAGTTGG 25	QY	1 GTTCAGCTTTTGTACAAAGTTGG 25
Db	40 GTTCAGCTTTTGTACAAAGTTGG 64	Db	40 GTTCAGCTTTTGTACAAAGTTGG 64
RESULT 28		RESULT 28	
US-08-728-785A-18		US-08-728-785A-18	
Sequence 18, Application US/08728785A		Sequence 18, Application US/08728785A	
Patent No. 5817506		Patent No. 5817506	
GENERAL INFORMATION:		GENERAL INFORMATION:	
APPLICANT:	Okano, Kazunori	APPLICANT:	Okano, Kazunori
TITLE OF INVENTION:	POLYNUCLEOTIDE CAPTURING TIP AND	TITLE OF INVENTION:	POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION:	POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION	TITLE OF INVENTION:	POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION:	METHOD USING SAME	TITLE OF INVENTION:	METHOD USING SAME
NUMBER OF SEQUENCES:	18	NUMBER OF SEQUENCES:	18
CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Antonelli, Terry, Stout & Kraus	ADDRESSEE:	Antonelli, Terry, Stout & Kraus
STREET:	Suite 1800, 1300 No. 5817506th Seventeenth St.	STREET:	Suite 1800, 1300 No. 5817506th Seventeenth St.
CITY:	Arlington	CITY:	Arlington
STATE:	VA	STATE:	VA
COUNTRY:	USA	COUNTRY:	USA
ZIP:	22209	ZIP:	22209
COMPUTER READABLE FORM:		COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk	MEDIUM TYPE:	Floppy disk
OPERATING SYSTEM:	PC-DOS/MS-DOS	OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.25	SOFTWARE:	PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER:	US/08/728,785A	APPLICATION NUMBER:	US/08/728,785A
FILING DATE:	10-OCT-1996	FILING DATE:	10-OCT-1996
CLASSIFICATION:	435	CLASSIFICATION:	435
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/410,544	APPLICATION NUMBER:	08/410,544
FILING DATE:	21-MAR-1995	FILING DATE:	21-MAR-1995
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/021,667	APPLICATION NUMBER:	08/021,667
FILING DATE:	24-FEB-1993	FILING DATE:	24-FEB-1993
ATTORNEY/AGENT INFORMATION:		ATTORNEY/AGENT INFORMATION:	
NAME:	Terry, David T.	NAME:	Terry, David T.
REGISTRATION NUMBER:	20,178	REGISTRATION NUMBER:	20,178
REFERENCE/DOCKET NUMBER:	520.31930X00	REFERENCE/DOCKET NUMBER:	520.31930X00
TELEPHONE:	703-312-6600	TELEPHONE:	703-312-6600
TELEFAX:	703-312-6666	TELEFAX:	703-312-6666
INFORMATION FOR SEQ ID NO:	18:	INFORMATION FOR SEQ ID NO:	18:
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH:	201 base pairs	LENGTH:	201 base pairs
TYPE:	nucleic acid	TYPE:	nucleic acid
STRANDEDNESS:	single	STRANDEDNESS:	single
TOPOLOGY:	linear	TOPOLOGY:	linear

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0

QY 1 GTTCAGCTTTTCTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTCTGTACAAAGTTG 24
   |||||

RESULT 32
US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna

```

US-09-005-476-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 33

US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 34

US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 35

US-09-296-280-11
; Sequence 11, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 36

US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264

```

;
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-10

Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 37
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

```

```

;
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-10

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTCTGTACAAACTTG 24

RESULT 38
US-09-233-493-5
; Sequence 5, Application US/09233493
; Patent No. 6,435,57
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-5

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 5.8;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 39
US-09-233-493-12
; Sequence 12, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-12

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||:
Db 4 CAGCTTTTGTACAAAGTTGG 25

Search completed: November 7, 2003, 00:22:53
Job time : 29 secs

Db 4 CTGCTTTTGTACAAAGTTGG 25

RESULT 40
US-09-233-493-14
; Sequence 14, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-14

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||:
Db 4 CAGCTTTTGTACAAAGTTGG 25

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:12:53 ; Search time 28 Seconds

(without alignments)
394.092 Million cell updates/sec

Title: US-10-055-001A-11

Perfect score: 25

Sequence: 1 gttcagcttctgtacaaagtgg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3	US-09-233-493-11
2	25	100.0	25	3	US-09-233-493-16
3	25	100.0	25	3	US-09-005-476-11
4	25	100.0	25	3	US-09-005-476-16
5	25	100.0	25	3	US-09-233-492-11
6	25	100.0	25	3	US-09-233-492-16
7	25	100.0	25	3	US-09-296-280-16
8	25	100.0	25	4	US-09-498-074-11
9	25	100.0	25	4	US-09-498-074-16
10	25	100.0	25	5	PCT-US96-10082A-11
11	25	100.0	25	5	PCT-US96-10082A-16
12	23.8	95.2	25	3	US-09-296-280-43
13	23.4	93.6	25	3	US-09-233-493-15
14	23.4	93.6	25	3	US-09-005-476-15
15	23.4	93.6	25	3	US-09-233-492-15
16	23.4	93.6	25	3	US-09-296-280-15
17	23.4	93.6	25	4	US-09-498-074-15
18	23.4	93.6	25	5	PCT-US96-10082A-15
19	22.4	89.6	25	3	US-09-233-493-10
20	22.4	89.6	25	3	US-09-005-476-10
21	22.4	89.6	25	3	US-09-233-492-10
22	22.4	89.6	25	3	US-09-296-280-10
23	22.4	89.6	25	3	US-09-236-280-11
24	22.4	89.6	25	4	US-09-498-074-10
25	22.4	89.6	25	5	PCT-US96-10082A-10
26	22	88.0	25	3	US-09-233-493-14
27	22	88.0	25	3	US-09-005-476-14

28	22	88.0	25	3	US-09-233-492-14	Sequence 14, Appl
29	22	88.0	25	3	US-09-296-280-14	Sequence 14, Appl
30	22	88.0	25	3	US-09-296-280-42	Sequence 42, Appl
31	22	88.0	25	4	US-09-498-074-14	Sequence 14, Appl
32	22	88.0	25	5	PCT-US96-10082A-14	Sequence 14, Appl
33	20.8	83.2	25	3	US-09-233-493-9	Sequence 9, Appl
34	20.8	83.2	25	3	US-09-005-476-9	Sequence 9, Appl
35	20.8	83.2	25	3	US-09-233-492-9	Sequence 9, Appl
36	20.8	83.2	25	3	US-09-296-280-9	Sequence 9, Appl
37	20.8	83.2	25	4	US-09-498-074-9	Sequence 9, Appl
38	20.8	83.2	25	5	PCT-US96-10082A-9	Sequence 9, Appl
39	20.4	81.6	25	3	US-09-233-493-5	Sequence 5, Appl
40	20.4	81.6	25	3	US-09-233-493-13	Sequence 13, Appl
41	20.4	81.6	25	3	US-09-005-476-5	Sequence 5, Appl
42	20.4	81.6	25	3	US-09-005-476-13	Sequence 13, Appl
43	20.4	81.6	25	3	US-09-233-492-5	Sequence 5, Appl
44	20.4	81.6	25	3	US-09-233-492-13	Sequence 13, Appl
45	20.4	81.6	25	3	US-09-296-280-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-233-493-11
; Sequence 11, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-11

Db 1 GTTCAGCTTCTTGTAACAAGTTGG 25
|||||
RESULT 6
US-09-233-492-16
; Sequence 16, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-16
Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTTGTAACAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTAACAAGTTGG 25
|||||
RESULT 7
US-09-296-280-16
; Sequence 16, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

Qy 1 GTTCAGCTTCTTGTAACAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTAACAAGTTGG 25
|||||
RESULT 5
US-09-233-492-11
; Sequence 11, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-11
Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTTGTAACAAGTTGG 25
|||||

; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 16
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 US-09-296-280-16

Query Match 100.0%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 8
 US-09-498-074-11
 ; Sequence 11, Application US/09498074
 ; Patent No. 6534264
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/498,074
 ; FILING DATE: (Herewith)
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2540
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 US-09-498-074-11

Query Match 100.0%; Score 25; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 9
 US-09-498-074-16
 ; Sequence 16, Application US/09498074
 ; Patent No. 6534264
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/498,074
 ; FILING DATE: (Herewith)
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2540
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 US-09-498-074-16

Query Match 100.0%; Score 25; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 10
 PCT-US96-10082A-11
 ; Sequence 11, Application PC/TUS9610082A
 ; GENERAL INFORMATION:

Fri Nov 7 08:08:38 2003

APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
PCT-US96-10082A-11

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 11
PCT-US96-10082A-16
Sequence 16 Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
PCT-US96-10082A-16

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 12
US-09-296-280-43
Sequence 43 Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296.280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 43
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-43

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.051;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 13
US-09-233-493-15
Sequence 15 Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington

us-10-055-001a-11.rni

Fri Nov 7 08:08:38 2003

```
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-15

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAAAGTTGG 25
   |||||||
Db 1 GTTCAGCTTTTTGTACAAAGTTGG 25

RESULT 15
US-09-233-492-15
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-15

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAAAGTTGG 25
   |||||||
Db 1 GTTCAGCTTTTTGTACAAAGTTGG 25

RESULT 14
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
```

Fri Nov 7 08:08:38 2003

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

RESULT 16
US-09-296-280-15
; Sequence 15, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942,2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-15

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

RESULT 17
US-09-498-074-15
; Sequence 15, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-15

Query Match 93.6%; Score 23.4; DB 4; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

RESULT 18
PCT-US96-10082A-15
; Sequence 15, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
PCT-US96-10082A-15

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTGACAAAGTTG 25
RESULT 19
US-09-233-493-10
; Sequence 10, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-10
Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTGACAAAGTTG 24
Db 1 GTTCAGCTTTTGTGACAAAGTTG 24
RESULT 21
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-10
Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTGACAAAGTTG 24
Db 1 GTTCAGCTTTTGTGACAAAGTTG 24
RESULT 20
US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35

us-10-055-001a-11.ini

Fri Nov 7 08:08:38 2003

```

; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-492-10

Query Match      89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 22
US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQUENCE ID NO: 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-296-280-10

Query Match      89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 24
US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA

```

```
US-09-498-074-10
Query Match      89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTCTGTGTACAAAGTTG 24

RESULT 25
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-10

Query Match      89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTGTACAAAGTTG 24
    |||||
Db 1 GTTCAGCTTTCTGTGTACAAAGTTG 24

RESULT 26
US-09-233-493-14
; Sequence 14, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-14

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTCTGTGTACAAAGTTG 25
    |||||
Db 4 CAGCTTTCTGTGTACAAAGTTG 25

RESULT 27
US-09-005-476-14
; Sequence 14, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-14
```


APPLICATION NUMBER: 08/663,002
 FILING DATE: 07-JUN-1996
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 US-09-005-476-14

Query Match 88.0%; Score 22; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 4 CAGCTTCTTGTACAAAGTTGG 25

RESULT 28
 US-09-233-492-14
 ; Sequence 14, Application US/09233492
 ; Patent No. 6270969
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,492
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 US-09-233-492-14

Query Match 88.0%; Score 22; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 4 CAGCTTCTTGTACAAAGTTGG 25

RESULT 29
 US-09-296-280-14
 ; Sequence 14, Application US/09296280
 ; Patent No. 6277608
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 ; TITLE OF INVENTION: Recombination Sites
 ; FILE REFERENCE: 0942.2850007
 ; CURRENT APPLICATION NUMBER: US/09/296,280
 ; CURRENT FILING DATE: 1999-04-22
 ; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; TYPE: DNA
 ; LENGTH: 25
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 US-09-296-280-14

Query Match 88.0%; Score 22; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTACAAAGTTGG 25
 |||||
 Db 4 CAGCTTCTTGTACAAAGTTGG 25

RESULT 30
 US-09-296-280-42
 ; Sequence 42, Application US/09296280
 ; Patent No. 6277608
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 ; TITLE OF INVENTION: Recombination Sites
 ; FILE REFERENCE: 0942.2850007
 ; CURRENT APPLICATION NUMBER: US/09/296,280
 ; CURRENT FILING DATE: 1999-04-22
 ; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 42
 ; TYPE: DNA
 ; LENGTH: 25
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 US-09-296-280-42

Query Match 88.0%; Score 22; DB 3; Length 25;

Best Local Similarity 79.2%; Pred. No. 0.33; Mismatches 5; Conservative 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTGTACAAAGTTG 24
Db 1 GTTCAGCTTCTGTACAAAGTTG 24

RESULT 31
US-09-498-074-14
; Sequence 14, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-14

Query Match 88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTGTACAAAGTTG 25
Db 4 CAGCTTCTGTACAAAGTTG 25

RESULT 32
PCT-US96-10082A-14
; Sequence 14, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle

APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States Of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
PCT-US96-10082A-14

Query Match 88.0%; Score 22; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTGTACAAAGTTG 25
Db 4 CAGCTTCTGTACAAAGTTG 25

RESULT 33
US-09-233-493-9
; Sequence 9, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:

; PRIOR APPLICATION DATA: 83.2%; Score 20.8; DB 3; Length 25;
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-233-493-9

Query Match 83.2%; Score 20.8; DB 3; Length 25;
 Best Local Similarity 91.7%; Pred. No. 1.1;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTACAAAGTTG 24
 Db 1 GTTCAGCTTTCTGTACAAAGTTG 24

RESULT 34
 US-09-005-476-9
 ; Sequence 9, Application US/09005476
 ; Patent No. 6171861
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/005,476
 ; FILING DATE: herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-005-476-9

Query Match 83.2%; Score 20.8; DB 3; Length 25;
 Best Local Similarity 91.7%; Pred. No. 1.1;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTACAAAGTTG 24
 Db 1 GTTCAGCTTTCTGTACAAAGTTG 24

RESULT 35
 US-09-233-492-9
 ; Sequence 9, Application US/09233492
 ; Patent No. 6270969
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,492
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-233-492-9

Query Match 83.2%; Score 20.8; DB 3; Length 25;
 Best Local Similarity 91.7%; Pred. No. 1.1;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTACAAAGTTG 24
 Db 1 GTTCAGCTTTCTGTACAAAGTTG 24

RESULT 36
 US-09-296-280-9
 ; Sequence 9, Application US/09296280
 ; Patent No. 6277608
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; APPLICANT: Temple, Gary F.
 ; APPLICANT: Fox, Donna K.
 ; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 ; TITLE OF INVENTION: Recombination Sites
 ; FILE REFERENCE: 0942.2850007

;; CURRENT APPLICATION NUMBER: US/09/296,280
;; CURRENT FILING DATE: 1999-04-22
;; EARLIER APPLICATION NUMBER: US 09/177,387
;; EARLIER FILING DATE: 1998-10-23
;; EARLIER APPLICATION NUMBER: US 60/065,930
;; EARLIER FILING DATE: 1997-10-24
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 9
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Unknown
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: recombination
;; OTHER INFORMATION: products
US-09-296-280-9

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTTGACAAAGTTG 24
|||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 37
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both

;; MOLECULE TYPE: CDNA
US-09-498-074-9
Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTTGACAAAGTTG 24
|||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 38
PCT-US96-10082A-9
; Sequence 9, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
PCT-US96-10082A-9

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTTGACAAAGTTG 24
|||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 39
US-09-233-493-5
; Sequence 5, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

```

; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-5

```

```

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.7;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

```

```

RESULT 40
US-09-233-493-13
; Sequence 13, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-493-13

```

```

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4 CAGCTTTCTTGTACAAAGTTGG 25
Db 4 CTGCTTTCTTGTACAAAGTTGG 25

```

```

Search completed: November 7, 2003, 00:22:53
Job time : 28 secs

```



```

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAACTTGT 25
    |||||
Db 1 GTTCAGCTTTCTTGTCACAACTTGT 25

RESULT 2
US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-10

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAACTTGT 25
    |||||
Db 1 GTTCAGCTTTCTTGTCACAACTTGT 25

RESULT 3
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington

```

```

; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-10

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAACTTGT 25
    |||||
Db 1 GTTCAGCTTTCTTGTCACAACTTGT 25

RESULT 4
US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942 2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 5
US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-10

Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 6
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 7
US-09-233-493-9
; Sequence 9, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25


```

; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-9

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 8
US-09-005-476-9
; Sequence 9, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-9

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 9
US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-9

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 10
US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
;

```

EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
TYPE: DNA
LENGTH: 25
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-9

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 11
US-09-498-074-9
Sequence 9, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-498-074-9

Query Match 93.6%; Score 23.4; DB 4; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 12
PCT-US96-10082A-9
Sequence 9, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
PCT-US96-10082A-9

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 13
US-09-296-280-42
Sequence 42, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22

; EARLIER APPLICATION NUMBER: US 09/177,387
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: US 60/065,930
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 42
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: recombination
 ; OTHER INFORMATION: products
 ; US-09-296-280-42

Query Match 90.4%; Score 22.6; DB 3; Length 25;
 Best Local Similarity 76.0%; Pred. No. 0.15;
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTGACAACTTGT 25
 |||||
 Db 1 GTTCAGCTTTCTGTGACAACTTGT 25

RESULT 14
 US-09-233-493-11
 ; Sequence 11, Application US/09233493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,493
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-233-493-11

Query Match 89.6%; Score 22.4; DB 3; Length 25;
 Best Local Similarity 95.8%; Pred. No. 0.18;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTGACAACTTGT 24
 |||||
 Db 1 GTTCAGCTTTCTGTGACAACTTGT 24

RESULT 15
 US-09-233-493-16
 ; Sequence 16, Application US/09233493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/233,493
 ; FILING DATE: 20-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cdna
 ; US-09-233-493-16

Query Match 89.6%; Score 22.4; DB 3; Length 25;
 Best Local Similarity 95.8%; Pred. No. 0.18;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTGACAACTTGT 24
 |||||
 Db 1 GTTCAGCTTTCTGTGACAACTTGT 24

RESULT 16
 US-09-005-476-11
 ; Sequence 11, Application US/09005476
 ; Patent No. 6171861

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-005-476-11

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAAACTTG 24
|||||
DB 1 GTTCAGCTTTCTTTGTACAAAGTTG 24
|||||

RESULT 17
US-09-005-476-16
Sequence 16, Application US/09005476
Patent No. 6171961
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-005-476-16

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTTGTACAAACTTG 24
|||||
DB 1 GTTCAGCTTTCTTTGTACAAAGTTG 24
|||||

RESULT 18
US-09-233-492-11
Sequence 11, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-11

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```
US-09-498-074-11
Query Match      89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAAACTTG 24
   |||||
Db 1 GTTCAGCTTCTGTGACAAAGTTG 24

RESULT 22
US-09-498-074-16
; Sequence 16, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/563,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-16

Query Match      89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAAACTTG 24
   |||||
Db 1 GTTCAGCTTCTGTGACAAAGTTG 24

RESULT 23
PCT-US96-10082A-11
; Sequence 11, Application PC/TUS9610082A
```

```
GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-11

Query Match      89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAAACTTG 24
   |||||
Db 1 GTTCAGCTTCTGTGACAAAGTTG 24

RESULT 24
PCT-US96-10082A-16
; Sequence 16, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
```

CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
PCT-US96-10082A-16

Query Match 89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTACAACTTG 24
DB 1 GTTCAGCTTCTGTACAAAGTIG 24

RESULT 25
US-09-233-493-8
; Sequence 8, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-8

Query Match 88.0%; Score 22; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTCTTGTACAACTTGT 25
DB 4 CAGCTTCTTGTACAACTTGT 25

RESULT 26
US-09-005-476-8
; Sequence 8, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-005-476-8

Query Match 88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CAGCTTCTTGTACAACTTGT 25
DB 4 CAGCTTCTTGTACAACTTGT 25

RESULT 27
US-09-233-492-8
; Sequence 8, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
US-09-233-492-8

```

; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-492-8

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTCTGTACAACTTGT 25
Db 4 CAGCTTCTCTGTACAACTTGT 25

RESULT 28
PCT-US96-10082A-8
; Sequence 8, Application US/09498074
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996

; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-8

Query Match      88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTCTGTACAACTTGT 25
Db 4 CAGCTTCTCTGTACAACTTGT 25

RESULT 29
PCT-US96-10082A-8
; Sequence 8, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-8

Query Match      88.0%; Score 22; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTCTCTGTACAACTTGT 25
Db 4 CAGCTTCTCTGTACAACTTGT 25
```


;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/233,493
;; FILING DATE: 20-JAN-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: CDNA
;; US-09-233-493-15

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTG 24
Db 1 GTTCAGCTTTCTTGACAACTTG 24

RESULT 34
US-09-005-476-3
; Sequence 3, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/005,476
;; FILING DATE: herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: CDNA
;; US-09-005-476-3

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTG 25
Db 1 GTTCAGCTTTCTTGACAACTSG 25

RESULT 35
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-15

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTG 24

Db 1 GTTCAGCTTTTGTGACAAAGTTG 24
|||||

RESULT 36
US-09-233-492-3
; Sequence 3, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-3

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTGACAAACTTGT 25
|||||

Db 1 GTTCAGCTTTCTGTGACAACTSGB 25
|||||

RESULT 37
US-09-233-492-15
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-15

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTGACAAACTTG 24
|||||

Db 1 GTTCAGCTTTTGTGACAAAGTTG 24
|||||

RESULT 38
US-09-296-280-3
; Sequence 3, Application US/09296280
; Patent No. 627608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007 US/09/296,280
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: Products
US-09-296-280-3

40 98-074-3 Application US/09498074
 Patent No. 6534264
 SERIAL INFORMATION:
 APPLICANT: Hartley, Michael A.
 INVENTOR: Bransch, Michael A.
 TITLE OF INVENTION: Recombinational Cloning Using Engineered
 Plasmids
 NUMBER OF INVENTION: Recombination Sites
 NUMBER OF SEQUENCES: 35
 ADDRESS:
 ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 STREET: 1100 New York Ave., N. W. Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/498,074
 FILING DATE: (Herewith)
 CLASSIFICATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:12:53 : Search time 28 Seconds
(without alignments)
394.092 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaacttgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCITUS COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	100.0	25	3	US-09-233-493-9
2	25	100.0	25	3	US-09-005-476-9
3	25	100.0	25	3	US-09-233-492-9
4	25	100.0	25	3	US-09-233-492-9
5	25	100.0	25	4	US-09-296-280-9
6	25	100.0	25	5	US-09-498-074-9
7	23.4	93.6	25	3	PCT-US96-10082A-9
8	23.4	93.6	25	3	US-09-233-493-10
9	23.4	93.6	25	3	US-09-005-476-10
10	23.4	93.6	25	3	US-09-233-492-10
11	23.4	93.6	25	4	US-09-296-280-10
12	23.4	93.6	25	5	US-09-498-074-10
13	22.6	90.4	25	3	PCT-US96-10082A-10
14	22.4	89.6	25	3	US-09-286-280-42
15	22.4	89.6	25	3	US-09-233-493-15
16	22.4	89.6	25	3	US-09-005-476-15
17	22.4	89.6	25	3	US-09-233-492-15
18	22.4	89.6	25	3	US-09-296-280-15
19	22.4	89.6	25	4	US-09-498-074-15
20	21.2	84.8	25	5	PCT-US96-10082A-15
21	20.8	83.2	25	3	US-09-296-280-43
22	20.8	83.2	25	3	US-09-233-493-11
23	20.8	83.2	25	3	US-09-233-493-16
24	20.8	83.2	25	3	US-09-005-476-11
25	20.8	83.2	25	3	US-09-005-476-16
26	20.8	83.2	25	3	US-09-233-492-11
27	20.8	83.2	25	3	US-09-233-492-16
					Sequence 16, Appl

28	20.8	83.2	25	4	US-09-498-074-11	Sequence 11, Appl
29	20.8	83.2	25	4	US-09-498-074-16	Sequence 16, Appl
30	20.8	83.2	25	5	PCT-US96-10082A-11	Sequence 11, Appl
31	20.8	83.2	25	5	PCT-US96-10082A-16	Sequence 16, Appl
32	20.4	81.6	25	3	US-09-233-493-6	Sequence 6, Appl
33	20.4	81.6	25	3	US-09-233-493-8	Sequence 8, Appl
34	20.4	81.6	25	3	US-09-233-493-33	Sequence 33, Appl
35	20.4	81.6	25	3	US-09-005-476-6	Sequence 6, Appl
36	20.4	81.6	25	3	US-09-005-476-8	Sequence 8, Appl
37	20.4	81.6	25	3	US-09-005-476-33	Sequence 33, Appl
38	20.4	81.6	25	3	US-09-233-492-6	Sequence 6, Appl
39	20.4	81.6	25	3	US-09-233-492-8	Sequence 8, Appl
40	20.4	81.6	25	3	US-09-233-492-33	Sequence 33, Appl
41	20.4	81.6	25	3	US-09-296-280-6	Sequence 6, Appl
42	20.4	81.6	25	4	US-09-498-074-6	Sequence 6, Appl
43	20.4	81.6	25	4	US-09-498-074-8	Sequence 8, Appl
44	20.4	81.6	25	4	US-09-498-074-33	Sequence 33, Appl
45	20.4	81.6	25	5	PCT-US96-10082A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-233-493-9
: Sequence 9, Application US/09233493
: Patent No. 6143557
: GENERAL INFORMATION:
: APPLICANT: Hartley, James L.
: APPLICANT: Brasch, Michael A.
: TITLE OF INVENTION: Recombinational Cloning Using Engineered
: TITLE OF INVENTION: Recombination Sites
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
: STREET: 1100 New York Ave., N. W. Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/233,493
: FILING DATE: 20-JAN-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/005,476
: FILING DATE: 12-JAN-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/663,002
: FILING DATE: 07-JUN-1996
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/486,139
: FILING DATE: 07-JUN-1995
: CLASSIFICATION:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: cdna
US-09-233-493-9

```
Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 2
US-09-005-476-9
; Sequence 9, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2600
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-9

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 3
US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
```

```
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-9

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 4
US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-9

Query Match      100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 5
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-9

Query Match 100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 6
PCT-US96-10082A-9
; Sequence 9, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20894-9980
; APPLICANT: United States of America

```

```

; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-9

Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 7
US-09-233-493-10
; Sequence 10, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002

```

; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-10

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 8
US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-10

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25

Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 9
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-10

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 10
US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match 93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTCTGTACAAACTTGT 25

RESULT 11
US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-10

Query Match 93.6%; Score 23.4; DB 4; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTCTGTACAAACTTGT 25

RESULT 12
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
PCT-US96-10082A-10

Query Match 93.6%; Score 23.4; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTCTGTACAAACTTGT 25

RESULT 13
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.71;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
|||
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 14
US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 15
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 16
US-09-233-492-15
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTG 24
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 17
US-09-296-280-15
Sequence 15, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-15

Query Match 89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTTGTACAACTTG 24
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 18
US-09-498-074-15
Sequence 15, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-498-074-15

Query Match 89.6%; Score 22.4; DB 4; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTG 24
Db 1 GTTCAGCTTTTGTACAACTTG 24

RESULT 19
PCT-US96-10082A-15
Sequence 15, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980

APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
SITE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
PCT-US96-10082A-15

Query Match 89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 20
US-09-296-280-43
Sequence 43, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
SITE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-43
Query Match 84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.6;

Matches 20; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 21
US-09-233-493-11
Sequence 11, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
SITE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-233-493-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 22
US-09-233-493-16
Sequence 16, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.

;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/233,493
;; FILING DATE: 20-JAN-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-233-493-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 23
US-09-005-476-11
;; Sequence 11, Application US/09005476
;; Patent No. 6171861
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/09/005,476
;; FILING DATE: herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-005-476-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 24
US-09-005-476-16
;; Sequence 16, Application US/09005476
;; Patent No. 6171861
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/09/005,476
;; FILING DATE: herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-005-476-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 25

US-09-233-492-11
; Sequence 11, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-11

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 26

US-09-233-492-16
; Sequence 16, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-233-492-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTG 24
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 27

US-09-296-280-16
; Sequence 16, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: Products
US-09-296-280-16

Query Match 83.2%; Score 20.8; DB 3; Length 25;

Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 28

US-09-498-074-11
; Sequence 11, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-11

Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 29

US-09-498-074-16
; Sequence 16, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-16

Query Match 83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 30

PCT-US96-10082A-11
; Sequence 11, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10082A
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2540
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
PCT-US96-10082A-11

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
Db 1 GTTCAGCTTCTGTACAAAGTTG 24

RESULT 31
PCT-US96-10082A-16
;; Sequence 16, Application PC/TUS9610082A
;; GENERAL INFORMATION:
;; APPLICANT: Life Technologies, Inc.
;; APPLICANT: 8717 Grovemont Circle
;; APPLICANT: Gaithersburg, MD 20884-9980
;; APPLICANT: United States of America
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10082A
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
PCT-US96-10082A-16

Query Match 83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
Db 1 GTTCAGCTTCTGTACAAAGTTG 24

RESULT 32
US-09-233-493-6
;; Sequence 6, Application US/09233493
;; Patent No. 6143557
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/233,493
;; FILING DATE: 20-JAN-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-233-493-6

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAACTTGT 25
|||||
Db 4 CTGCTTTTGTACAACTTGT 25

RESULT 33
US-09-233-493-8
;; Sequence 8, Application US/09233493
;; Patent No. 6143557
;; GENERAL INFORMATION:
;; APPLICANT: Hartley, James L.
;; APPLICANT: Brasch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-8

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred.No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 CAGCTTTTGTACAAACTTGT 25

RESULT 34
US-09-233-493-33/c
Sequence 33, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-33

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred.No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 22 CTGCTTTTGTACAAACTTGT 1

RESULT 35
US-09-005-476-6
Sequence 6, Application US/09005476
Patent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

```
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-6

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25
   |||||
Db 4 CTGCTTTTGTACAAACTTGT 25

RESULT 36
US-09-005-476-8
; Sequence 8, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-33

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25
   |||||
Db 22 CTGCTTTTGTACAAACTTGT 1

RESULT 38
US-09-233-492-6
; Sequence 6, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
```

CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-492-6

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
Db 4 CTGCTTTTGTACAAACTTGT 25

RESULT 39
US-09-233-492-8
; Sequence 8, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-492-8

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 4 CAGCTTTTGTACAAACTTGT 25

RESULT 40
US-09-233-492-33/C
; Sequence 33, Application US/092333492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-492-33

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25
Db 22 CTGCTTTTGTACAAACTTGT 1

Search completed: November 7, 2003, 00:22:52
Job time : 28 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:05:38 ; Search time 111.5 Seconds
(without alignments)
605.255 Million cell updates/sec

Title: US-10-055-001a-11

Perfect score: 25

Sequence: 1 gttcagctttctgtacaaagtgg 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq 19Jun03*

1: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT.*
25: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	18	attP2,P3 core regi
2	25	100.0	25	20	Oligonucleotide #1
3	25	100.0	25	22	Recombination site
4	25	100.0	25	22	Recombination site
5	25	100.0	25	22	Recombination site
6	25	100.0	25	22	Recombination site
7	25	100.0	25	22	Recombination site
8	25	100.0	25	22	Escherichia coli c

9	25	100.0	25	23	AA514785
10	25	100.0	25	24	ABQ82123
11	25	100.0	25	24	ABQ82128
12	25	100.0	25	25	ACC44660
13	25	100.0	25	25	ACC44665
14	25	100.0	25	25	ABT16630
15	25	100.0	25	25	ABT16635
16	25	100.0	25	25	ABT16635
17	25	100.0	27	22	AA506183
18	25	100.0	27	25	ABZ58736
19	25	100.0	233	21	AA55383
20	25	100.0	4165	21	AA55524
21	25	100.0	4204	21	AA55522
22	25	100.0	4208	21	AA55523
23	25	100.0	4428	25	ABZ58768
24	25	100.0	4470	21	AA55521
25	25	100.0	4470	21	ABZ58767
26	25	100.0	4627	25	ABZ58769
27	25	100.0	4627	25	ABZ58770
28	25	100.0	4939	21	AA55525
29	25	100.0	5156	21	AA55526
30	25	100.0	5584	21	AA55632
31	25	100.0	18691	24	ABQ82130
32	25	100.0	18691	24	ABQ82130
33	23.8	95.2	25	20	AA78977
34	23.4	93.6	25	18	AA748224
35	23.4	93.6	25	20	AA78949
36	23.4	93.6	25	22	AA55749
37	23.4	93.6	25	22	AA55749
38	23.4	93.6	25	22	AA55749
39	23.4	93.6	25	24	ABQ82127
40	23.4	93.6	25	25	ACC44664
41	23.4	93.6	25	25	ABT16634
42	23.4	93.6	25	25	ABT16634
43	23.4	93.6	27	22	AA506179
44	23.4	93.6	27	25	ABZ58732
45	23.4	93.6	233	21	AA55382
	23.4	93.6	4165	21	AA55524

ALIGNMENTS

RESULT 1

AA748225

ID AA748225 standard; DNA; 25 BP.

AC AA748225;

DT 20-OCT-1997 (first entry)

DE attP2,P3 core region.

DE att recombination site; core region; mutation; enhance; recombination;

KW vector; subcloning; regulation; exchange; ss.

OS Synthetic.

PN WO9640724-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US10082.

PR 07-JUN-1995; 95US-0486139.

PA (LIFE-) LIFE TECHNOLOGIES INC.

PI Brasch MA, Hartley JL;

DR WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

PT using recombinant proteins and methods to obtain recombination sites in

PT vitro or in vivo
XX
PS Claim 14; Page 56; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTTGACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25
RESULT 2
AAX78950
ID AAX78950 standard; DNA; 25 BP.
AC AAX78950;
XX
DT 17-AUG-1999 (first entry)
XX
DE Oligonucleotide #16 for recombination and cloning method.
XX
KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
OS Synthetic.
XX
EN WO9921977-A1.
XX
PD 06-MAY-1999.
XX
PF 26-OCT-1998; 98WO-US22589.
XX
PR 23-OCT-1998; 98US-0177387.
XX
PR 24-OCT-1997; 97US-0065930.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Fox DK, Hartley JL, Temple GF;
XX
DR WPI; 1999-303011/25.
XX
PT New nucleic acid cloning methods
XX
PS Disclosure; Page 163; 185pp; English.
XX
CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more
CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that

CC have the desired characteristics and/or nucleic acid segments. The
CC methods can also be used for changing vectors. The oligonucleotides
CC AAX78935-X78994 are used in the method of the invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTTGACAAAGTTGG 25
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25
RESULT 3
AAD14439
ID AAD14439 standard; DNA; 25 BP.
AC AAD14439;
XX
DT 01-NOV-2001 (first entry)
XX
DE Recombination site attR3 DNA.
XX
KW Recombination site; copy number; replicon; recombinatorial cloning;
XX attr3; ds.
XX
OS Unidentified.
XX
EN US6270969-B1.
XX
PD 07-AUG-2001.
XX
PF 20-JAN-1999; 99US-0233492.
XX
PR 07-JUN-1996; 96US-0663002.
XX
PR 07-JUN-1995; 95US-0486139.
XX
FA (INVI-) INVITROGEN CORP.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2001-488248/53.
XX
PT Methods for apposing nucleic acids comprising an expression signal and
PT a gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under
PT conditions for recombination -
XX
PS Claim 14; Column 18; 76pp; English.
XX
CC The invention relates to a method for apposing an expression signal and
CC a gene or partial gene, using recombinatorial cloning. The method
CC incubates nucleic acids comprising the expression signal and the gene/
CC partial gene in the presence of a recombination protein under conditions
CC sufficient to cause recombination and therefore appose the expression
CC signal and the gene or partial gene. The methods are useful for apposing
CC an expression signal and a gene or partial gene using recombinatorial
CC cloning. The methods are also useful for changing vectors, constructing
CC genes for fusion proteins, changing copy number, changing replicons,
CC cloning into phages, and cloning e.g., PCR products (with an attB site
CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
CC The methods are highly specific, rapid, and less labour intensive than
CC prior art methods. The present sequence is a recombination site
CC useful for recombination cloning.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Faraday Avenue Genoscope sequence ID : CS0DC002AC03QPI.

FEATURES

Location/Qualifiers

1..1190
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC002YB05"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 248 a 332 c 362 g 209 t 39 others

ORIGIN

Query Match 84.8%; Score 21.2; DB 13; Length 1190;
Best Local Similarity 90.9%; Pred. No. 5.5e+02;
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAACTTGT 25

Db 38 CWGCTTTTGTACAACTTGT 17

RESULT 38

AL541966/c

LOCUS

DEFINITION AL541966 Homo sapiens PLACENTA Homo sapiens cDNA clone EST 12-MAY-2003

5-PRIME, mRNA sequence.

ACCESSION AL541966

VERSION AL541966.2 GI:30546649

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12873543.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 8896.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DE007DA04QPI&cluster=8896.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DE007DA04QPI.

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DE007YB08"

/tissue_type="PLACENTA"

/clone_lib="Homo sapiens PLACENTA"

/note="vector: pCMVSPORT 6, 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

BASE COUNT 228 a 364 c 398 g 175 t 36 others

ORIGIN

Query Match

Best Local Similarity

Matches 20; Conservative

2; Mismatches

0; Indels

0; Gaps

0;

0;

0;

0;

0;

0;

0;

0;

0;

Qy 4 CAGCTTTTGTACAACTTGT 25

Db 31 CWGCTTTTGTACAACTTGT 10

RESULT 39

AL544813

LOCUS

DEFINITION

AL544813 Homo sapiens PLACENTA COT 25-NORMALIZED

clone CS0DI012YK20 3-PRIME, mRNA sequence.

ACCESSION

AL544813

VERSION

AL544813.2

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12877293.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 79.f For more

information about this cluster, see http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI012BF10NP1&cluster=79.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI012BF10NP1.

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI012YK20"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 324 a 240 c 255 g 315 t 67 others

ORIGIN

Query Match

Best Local Similarity

Matches 20; Conservative

2; Mismatches

0; Indels

0; Gaps

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

SOURCE

```

RESULT 32
BX417226/c
LOCUS
DEFINITION
  BX417226 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE006YI08
  S-PRIME, mRNA sequence.
ACCESSION
  BX417226
VERSION
  BX417226.1 GI:30658353
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 1201)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DE006B504QP1.
FEATURES
  source
  1..1201
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DE006YI08"
    /tissue_type="PLACENTA"
    /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
    with a NotI-oligo(dT) primer. Five prime end enriched,
    double-strand cDNA was digested with Not I and cloned into
    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
    Library was not normalized."
  BASE COUNT
    316 a 171 c 198 g 258 t 258 others
  ORIGIN
    1  GTTCAGCTTTTGTACAAACTTGT 25
    43  GNNCTGCTTTTGTACAAACTTGT 19

  Query Match      85.6%; Score 21.4; DB 13; Length 1201;
  Best Local Similarity 88.0%; Pred. No. 4.6e+02;
  Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY
  1  GTTCAGCTTTTGTACAAACTTGT 25
  43  GNNCTGCTTTTGTACAAACTTGT 19
  Db

RESULT 33
AL538458/c
LOCUS
DEFINITION
  AL538458 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
  CS0DF027YF04 5-PRIME, mRNA sequence.
ACCESSION
  AL538458
VERSION
  AL538458.2 GI:31263051
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 946)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  On Feb 13, 2001 this sequence version replaced gi:12801951.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 5628.f For

```

```

more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF027DH02QP1&cluster=5628.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF027DH02QP1.
FEATURES
  Location/Qualifiers
  1..946
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DF027YF04"
    /tissue_type="FETAL BRAIN"
    /dev stage="fetal"
    /clone_lib="Homo sapiens FETAL BRAIN"
    /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
    was primed with a NotI-oligo(dT) primer. Five prime end
    enriched, double-strand cDNA was digested with Not I and
    cloned into the Not I and EcoRV sites of the pCMVSPORT 6
    vector. Library was not normalized."
  BASE COUNT
    200 a 322 c 277 g 145 t 2 others
  ORIGIN
    1  CAGCTTTTGTACAAACTTGT 25
    36  CAGCTTTTGTACAAACTTGT 15

  Query Match      84.8%; Score 21.2; DB 9; Length 946;
  Best Local Similarity 95.5%; Pred. No. 5.4e+02;
  Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

  QY
  4  CAGCTTTTGTACAAACTTGT 25
  36  CAGCTTTTGTACAAACTTGT 15
  Db

RESULT 34
BX445504/c
LOCUS
DEFINITION
  BX445504 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
  CS0DA005YA10 5-PRIME, mRNA sequence.
ACCESSION
  BX445504
VERSION
  BX445504.1 GI:30774336
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 995)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 3874.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS1DA002ZA08QP1&cluster=3874.r. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS1DA002ZA08QP1.
FEATURES
  Location/Qualifiers
  1..995
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DA005YA10"
    /tissue_type="NEUROBLASTOMA"
    /clone_lib="Homo sapiens NEUROBLASTOMA"
    /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
    with a NotI-oligo(dT) primer. Five prime end enriched,
    double-strand cDNA was digested with Not I and cloned into
    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
    Library was not normalized."

```


ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1132)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5630.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP004DE06QPI&cluster=5630.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CSOCAP004DE06QPI.

FEATURES
Location/Qualifiers
1..1132
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP004YJ12"
/tissue type="THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dN) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 262 a 233 c 241 g 307 t 89 others
ORIGIN

Query Match 85.6%; Score 21.4; DB 13; Length 1132;
Best Local Similarity 88.0%; Pred. No. 4.5e+02;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG T 25
:-|:|||||||:
DB 42 GCYCTGCTTTTGTACAACTTG T 18
:-|:|||||||:

RESULT 30
BX332991/c
LOCUS BX332991 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CSODC018YE19 5-PRIME, mRNA sequence.
ACCESSION BX332991
VERSION BX332991.1 GI:30308156
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4028.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODC018AC100P1
&cluster=4028.f. Contact : Feng Liang Email : fliang@lifetech.com
URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODC018AC100P1.

FEATURES
Location/Qualifiers
1..1201

/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="CS0DC018YE19"			
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"			
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"			
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."			
BASE COUNT	327 a	257 c	281 g
ORIGIN	48 others		
Query Match	85.6%	Score 21.4;	DB 13; Length 1201;
Best Local Similarity	95.7%	Pred. No. 4.6e+02;	
Matches 22;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY	3	TCAGCTTTTGTACAACTTGT	25
DB	39	TCTGCTTTTGTACAACTTGT	17
RESULT 31			
EX399404/c			
LOCUS			
DEFINITION	EX399404 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI075YH01 5-PRIME, mRNA sequence.	1201 bp	mRNA linear EST 13-MAY-2003
ACCESSION	EX399404	GI:30621878	
VERSION	EX399404.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li W.B., Gruber C., Jesse J., and Polayes D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 622.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI075CD01Q1P1&cluster=622.f. Contact : Peng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue Genoscope, sequence ID : CS0DI075CD01Q1P1. Location/Qualifiers 1. 1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DI075YH01" /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
BASE COUNT	254 a	316 c	356 g
ORIGIN	79 others		
Query Match	85.6%	Score 21.4;	DB 13; Length 1201;
Best Local Similarity	95.7%	Pred. No. 4.6e+02;	
Matches 22;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10184.r For
more information about this cluster, see

[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK013CF02NM1&cluster=10184.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK013CF02NM1&cluster=10184.r). Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAK013CF02NM1.

FEATURES

Location/Qualifiers
1..1035

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC005YB15"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
3 others

BASE COUNT 173 a 260 c 217 g 382 t
ORIGIN
Query Match 85.6%; Score 21.4; DB 13; Length 1035;
Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAAACTTGT 25
Db 389 TCTGCTTTTGTACAAACTTGT 411

RESULT 27
EX329663
LOCUS
DEFINITION BX329663 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC023YN14 3-PRIME, mRNA sequence.

ACCESSION BX329663

VERSION BX329663.1 GI:30340861

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9540.f For

more information about this cluster, see

<http://www.genoscope.cns.fr/>

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAK018DE01NM1.

Location/Qualifiers

1..1071

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC023YN14"

/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

Location/Qualifiers
1..1071

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC023YN14"

/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 181 a 318 c 250 g 314 t 8 others
ORIGIN

Query Match 85.6%; Score 21.4; DB 13; Length 1071;

Best Local Similarity 95.7%; Pred. No. 4.5e+02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAAACTTGT 25

Db 467 TCTGCTTTTGTACAAACTTGT 489

FEATURES

Location/Qualifiers
1..1119

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0CAP004YN12"

/tissue_type="THYMUS"

/clone_lib="Homo sapiens THYMUS"

/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and EcoRV sites of the pCMVSPORT 6 vector."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

Library was not normalized."

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM005YF22"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT      173 a      289 c      273 g      160 t
ORIGIN
Query Match      85.6%; Score 21.4; DB 13; Length 898;
Best Local Similarity 88.0%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 35 GNNCTGCTTTTGTACAACTTGT 11

RESULT 24
EX373524
LOCUS
DEFINITION
BX373524 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI053YF07 3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 953)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7650.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK059DB03NM1&cluster=7650.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0BAK059DB03NM1.
Location/Qualifiers
1..953
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI053YF07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      217 a      221 c      134 g      381 t
ORIGIN
Query Match      85.6%; Score 21.4; DB 13; Length 953;
Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAACTTGT 25
Db 407 TCTGCTTTTGTACAACTTGT 429

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM005YF22"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT      173 a      289 c      273 g      160 t
ORIGIN
Query Match      85.6%; Score 21.4; DB 13; Length 898;
Best Local Similarity 88.0%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 35 GNNCTGCTTTTGTACAACTTGT 11

RESULT 24
EX373524
LOCUS
DEFINITION
BX373524 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI053YF07 3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 953)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7650.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK059DB03NM1&cluster=7650.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0BAK059DB03NM1.
Location/Qualifiers
1..953
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI053YF07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      217 a      221 c      134 g      381 t
ORIGIN
Query Match      85.6%; Score 21.4; DB 13; Length 953;
Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAACTTGT 25
Db 407 TCTGCTTTTGTACAACTTGT 429

```

```

RESULT 25
EX372532
LOCUS
DEFINITION
BX372532 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
cDNA clone CSODR007YB13 3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 965)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3642.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK011BG11NM1&cluster=3642.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0BAK011BG11NM1.
Location/Qualifiers
1..965
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODR007YB13"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      188 a      258 c      194 g      323 t
ORIGIN
Query Match      85.6%; Score 21.4; DB 13; Length 965;
Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAACTTGT 25
Db 333 TCTGCTTTTGTACAACTTGT 355

RESULT 26
EX372606
LOCUS
DEFINITION
BX372606 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CSODC005YB15 3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1035)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

```

```

Query Match      86.4%; Score 21.6; DB 13; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25
    |:|||||
Db 39 CWGCTTTTGTACAAACTTGT 18

RESULT 21
BX463202/c
LOCUS BX463202 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CSODM008YI09 5-PRIME, mRNA sequence.
ACCESSION BX463202
VERSION BX463202.1 GI:31025494
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9373.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODM008AE05QP1&cluster=9373.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODM008AE05QF1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM008YI09"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/notes="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 253 a 318 c 262 g 291 t
ORIGIN
source

Query Match      86.4%; Score 21.6; DB 13; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAACTTGT 25
    |:|||||
Db 23 CWGCTTTTGTACAAACTTGT 2

RESULT 22
BX373155
LOCUS BX373155 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI015YF12 3-PRIME, mRNA sequence.
ACCESSION BX373155
VERSION BX373155.1 GI:30458167
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7793.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODM009DCL1QPI&cluster=7793.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODM009DCL1QPI.
Location/Qualifiers
1. .898
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI015YF12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 292 a 181 c 161 g 257 t
ORIGIN
source

Query Match      85.6%; Score 21.4; DB 13; Length 891;
Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAAACTTGT 25
    |:|||||
Db 691 TCTGCTTTTGTACAAACTTGT 713

RESULT 23
BX448442/c
LOCUS BX448442 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CSODM009YF22 5-PRIME, mRNA sequence.
ACCESSION BX448442
VERSION BX448442.1 GI:31019933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 898)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7793.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODM009DCL1QPI&cluster=7793.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODM009DCL1QPI.
Location/Qualifiers
1. .898
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI015YF12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 292 a 181 c 161 g 257 t
ORIGIN
source

Query Match      85.6%; Score 21.4; DB 13; Length 891;
Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAGCTTTTGTACAAACTTGT 25
    |:|||||
Db 691 TCTGCTTTTGTACAAACTTGT 713

RESULT 23
BX448442/c
LOCUS BX448442 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CSODM009YF22 5-PRIME, mRNA sequence.
ACCESSION BX448442
VERSION BX448442.1 GI:31019933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 898)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7793.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODM009DCL1QPI&cluster=7793.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODM009DCL1QPI.
Location/Qualifiers
1. .898
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI015YF12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 292 a 181 c 161 g 257 t
ORIGIN
source

```

DEFINITION BX363509 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 Homo sapiens cDNA clone CS0DL001YD08 5-PRIME, mRNA sequence.
 ACCESSION BX363509
 VERSION BX363509.1 GI:30376731
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2356.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DL001YD04QP1&cluster=2356.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DL001DB04QP1.

FEATURES

source
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DL001YD08"
 /cell_type="B CELLS (RAMOS CELL LINE)"
 /cell_line="RAMOS CELL LINE"
 /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 335 a 140 c 217 g 340 t 169 others
 ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 1201;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAACTTGT 25
 |:|||||
 Db 35 CMGCTTTTGTGACAACTTGT 14

RESULT 19
 BX386369/c
 LOCUS BX386369 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0DI071YA13 5-PRIME, mRNA sequence.
 ACCESSION BX386369
 VERSION BX386369.1 GI:30436794
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 95.r For more

information about this cluster, see http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS1A1018ZE07QP1&cluster=95.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS1A1018ZE07QP1.

FEATURES

source
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI071YA13"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 232 a 290 c 326 g 241 t 112 others
 ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 1201;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAACTTGT 25
 |:|||||
 Db 30 CMGCTTTTGTGACAACTTGT 9

RESULT 20

BX400983/c
 LOCUS BX400983 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DK005YD11 5-PRIME, mRNA sequence.
 ACCESSION BX400983
 VERSION BX400983.1 GI:30626325
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1089.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DK005YD11&cluster=1089.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK005YD11.

FEATURES

source
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK005YD11"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 283 a 315 c 336 g 239 t 28 others
 ORIGIN

```

Dr 191 91006 EVRI Cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5023.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI081CC06QPi&cluster=5023.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DI081CC06QPi.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI081YF11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      279 a   244 c   318 g   244 t   116 others
ORIGIN

Query Match      86.4%; Score 21.6; DB 9; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.8e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy      4  CAGCTTTTGTGACAACTGTG 25
      |||||
Db      33 CAGCTTTTGTGACAACTTGW 12

RESULT 18
BX363509/c
LOCUS
BX363509      1201 bp      mRNA      linear      EST 05-MAY-2000

```

Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI005B03QP1.

FEATURES

source

Location/Qualifiers
 1. .933
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI005YI06"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 254 a 212 c 238 g 227 t 2 others

BASE COUNT

ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 933;
 Best Local Similarity 95.5%; Pred. No. 3.7e+02;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAACTTGT 25

DB 38 CAGCTTTTGTACAACTTGT 17

RESULT 13

AL550767/c

LOCUS AL550767 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI056YC22 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Feb 15, 2001 this sequence version replaced gi:12888058.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 629.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI056BB11QP1&cluster=629.f. Contact :

Feng Liang Email: fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI056BB11QP1.

FEATURES

source

Location/Qualifiers
 1. .1060
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI056YC22"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 243 a 276 c 226 g 257 t 58 others

BASE COUNT

ORIGIN

Query Match 86.4%; Score 21.6; DB 9; Length 1060;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAACTTGT 25

DB 40 CAGCTTTTGTACAACTTGT 19

RESULT 14

BX338865/c

LOCUS

DEFINITION BX338865 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI064YH04 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5957.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI064DD02QP1&cluster=5957.f. Contact :

Feng Liang Email: fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI064DD02QP1.

FEATURES

source

Location/Qualifiers
 1. .1084
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI064YH04"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 207 a 276 c 314 g 250 t 37 others

BASE COUNT

ORIGIN

Query Match 86.4%; Score 21.6; DB 13; Length 1084;
 Best Local Similarity 95.5%; Pred. No. 3.8e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAACTTGT 25

DB 33 CAGCTTTTGTACAACTTGT 12

RESULT 15

BX463747/c

LOCUS

DEFINITION BX463747 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF003YB02 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 1198)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

VERSION AL538354.2 GI:31267


```

BX457051/c
LOCUS BX457051 956 bp mRNA linear EST 22-MAY-2003
DEFINITION BX457051 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YP02
5-PRIME, mRNA sequence.
ACCESSION BX457051
VERSION BX457051.1 GI:31034832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 956)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6437.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0CAP005DH01Q1P1&cluster=6437.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP005DH01Q1P1.

FEATURES
Location/Qualifiers
1..956
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP005YP02"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 209 a 286 c 234 g 220 t 7 others
ORIGIN
Query Match 87.2%; Score 21.8; DB 13; Length 956;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 40 GCTCTGCTTTTGTACAACTTGT 16

RESULT 8
BX422399/c
LOCUS BX422399 973 bp mRNA linear EST 13-MAY-2003
DEFINITION BX422399 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
CS0DM004YD15 5-PRIME, mRNA sequence.
ACCESSION BX422399
VERSION BX422399.1 GI:30655319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 973)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7333.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AS009ZC07Q1P1&cluster=7333.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AS009ZC07Q1P1.

FEATURES
Location/Qualifiers
1..1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM004YD15"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into

```

```

Invitrogen. This sequence belongs to sequence cluster 7228.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DM004CB08QP1&cluster=7228.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DM004CB08QP1.

FEATURES
Location/Qualifiers
1..973
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM004YD15"
/tissue_type="FETAL LIVER"
/dev stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 287 a 205 c 218 g 260 t 3 others
ORIGIN
Query Match 87.2%; Score 21.8; DB 13; Length 973;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 29 GCTCTGCTTTTGTACAACTTGT 5

RESULT 9
BX428996/c
LOCUS BX428996 1006 bp mRNA linear EST 15-MAY-2003
DEFINITION BX428996 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
clone CS0DG005YF18 5-PRIME, mRNA sequence.
ACCESSION BX428996
VERSION BX428996.1 GI:30780782
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1006)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7333.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AS009ZC07Q1P1&cluster=7333.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AS009ZC07Q1P1.

FEATURES
Location/Qualifiers
1..1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DG005YF18"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/clone_lib="RAMOS CELL LINE"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into

```

```

JOURNAL
COMMENT
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6911.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC019BC08QPI&cluster=6911.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DC019BC08QPI.

FEATURES
source
1. .1145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC019YE16"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      298 a      226 c      244 g      308 t      69 others
ORIGIN

Query Match      88.0%; Score 22; DB 13; Length 1145;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CAGCTTTTGTACAACTTGT 25
|||||
Db      39 CAGCTTTTGTACAACTTGT 18

RESULT 5
BX361644/c
LOCUS
DEFINITION
BX361644 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ001VF12 5-PRIME, mRNA sequence.
ACCESSION
BX361644
VERSION
BX361644.1 GI:30366552
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7763.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ001DC06QPI&cluster=7763.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DJ001DC06QPI.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ001VF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"

```

```

/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      278 a      308 c      341 g      205 t      69 others
ORIGIN

Query Match      88.0%; Score 22; DB 13; Length 1201;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CAGCTTTTGTACAACTTGT 25
|||||
Db      35 CAGCTTTTGTACAACTTGT 14

RESULT 6
AL519260/c
LOCUS
DEFINITION
AL519260 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CS0DA012YH14 5-PRIME, mRNA sequence.
ACCESSION
AL519260
VERSION
AL519260.2 GI:30538367
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DA012DD07QPI&cluster=3874.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DA012DD07QPI.

FEATURES
source
1. .914
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA012YH14"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

BASE COUNT      186 a      310 c      254 g      158 t      6 others
ORIGIN

Query Match      87.2%; Score 21.8; DB 9; Length 914;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAACTTGT 25
|||||
Db      39 GCTCTGCTTTTGTACAACTTGT 15

RESULT 7

```

Faraday Avenue Genoscope sequence ID : CS0BAK021BF12NM1.

FEATURES

source

Location/Qualifiers

1..996

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DD005YC15"

/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 212 a 291 c 107 g 373 t 13 others

ORIGIN

Query Match 89.6%; Score 22.4; DB 13; Length 996;

Best Local Similarity 95.8%; Pred. No. 1.8e+02;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTCAGCTTTTGTACAAACTTGT 25

Db 425 TTTCAGCTTTTGTACAAACTTGT 448

RESULT 2

EX441089/c

LOCUS

DEFINITION

EX441089 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone

CS0DF014YA08 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2850.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgf-bin/cluster.cgi?seq=CS0DF014BA04QP1&cluster=2850.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF014BA04QP1.

FEATURES

source

Location/Qualifiers

1..934

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF014YA08"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

BASE COUNT 233 a 233 c 278 g 189 t 1 others

ORIGIN

Query Match 88.0%; Score 22; DB 13; Length 934;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 35 CAGCTTTTGTACAAACTTGT 14

RESULT 3

EX359829/c

LOCUS

DEFINITION

EX359829 Homo sapiens PLACENTA COT 25-NORMALIZED

clone CS0DI062YG23 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6269.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgf-bin/cluster.cgi?seq=CS0DI062AD12QP1&cluster=6269.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI062AD12QP1.

FEATURES

source

Location/Qualifiers

1..1092

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI062YG23"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 237 a 268 c 322 g 207 t 58 others

ORIGIN

Query Match 88.0%; Score 22; DB 13; Length 1092;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAACTTGT 25

Db 36 CAGCTTTTGTACAAACTTGT 15

RESULT 4

EX394655/c

LOCUS

DEFINITION

EX394655 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED

clone CS0DC019YE16 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6269.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds
(without alignments)
555.531 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaacttgt 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic1:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_eston:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.4	89.6	996	13	BX329816
C 2	22	88.0	934	13	BX441089
C 3	22	88.0	1092	13	BX359829
C 4	22	88.0	1145	13	BX394655

C 5	22	88.0	1201	13	BX361644
C 6	21.8	87.2	914	9	AL519260
C 7	21.8	87.2	956	13	BX457051
C 8	21.8	87.2	973	13	BX422399
C 9	21.8	87.2	1006	13	BX428996
C 10	21.6	86.4	894	13	BX333971
C 11	21.6	86.4	897	9	AL538354
C 12	21.6	86.4	933	13	BX334648
C 13	21.6	86.4	1060	9	AL550767
C 14	21.6	86.4	1084	13	BX338865
C 15	21.6	86.4	1198	13	BX463747
C 16	21.6	86.4	1201	9	AL544923
C 17	21.6	86.4	1201	9	AL554071
C 18	21.6	86.4	1201	13	BX363509
C 19	21.6	86.4	1201	13	BX386369
C 20	21.6	86.4	1201	13	BX400983
C 21	21.6	86.4	1201	13	BX463202
C 22	21.4	85.6	891	13	BX373155
C 23	21.4	85.6	898	13	BX484442
C 24	21.4	85.6	953	13	BX373524
C 25	21.4	85.6	965	13	BX372532
C 26	21.4	85.6	1035	13	BX372606
C 27	21.4	85.6	1071	13	BX329663
C 28	21.4	85.6	1119	13	BX437057
C 29	21.4	85.6	1132	13	BX456900
C 30	21.4	85.6	1201	13	BX332991
C 31	21.4	85.6	1201	13	BX399404
C 32	21.4	85.6	1201	13	BX417226
C 33	21.2	84.8	946	9	AL538458
C 34	21.2	84.8	995	13	BX445504
C 35	21.2	84.8	1067	13	BX375648
C 36	21.2	84.8	1122	9	AL559630
C 37	21.2	84.8	1190	13	BX374761
C 38	21.2	84.8	1201	9	AL541966
C 39	21.2	84.8	1201	9	AL544813
C 40	21	84.0	612	13	BX355712
C 41	21	84.0	834	13	BX358772
C 42	21	84.0	906	13	BX418181
C 43	21	84.0	911	9	AL520832
C 44	21	84.0	935	13	BX367104
C 45	21	84.0	953	13	BX403441

ALIGNMENTS

RESULT 1
BX329816
LOCUS
DEFINITION
BX329816 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD005YC15 3-PRIME, mRNA sequence.
ACCESSION
BX329816.1 GI:30342879
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
1 (bases 1 to 996)
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4354.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK021BF12NM1&cluster=4354.f. Contact :
Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 204 BP; 80 A; 35 C; 31 G; 58 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 204;
Best Local Similarity 96.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
|||||
Db 184 GTTCAGCTTCTTGACAACTTGT 160

RESULT 40
AAC55476/c
ID AAC55476 standard; DNA; 204 BP.
XX
AC AAC55476;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST11 fragment nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
XX Example 13; Fig 31; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 204 BP; 60 A; 53 C; 50 G; 41 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 204;
Best Local Similarity 96.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
|||||
Db 181 GTTCAGCTTCTTGACAACTTGT 157

Search completed: November 6, 2003, 22:26:29
Job time : 112.5 secs

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX
SQ Sequence 153 BP; 50 A; 28 C; 40 G; 35 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 153;
Best Local Similarity 96.0%; Pred. No. 0.71;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
||||| ||||| ||||| ||||| |||||
Db 127 GTTCAGCTTTTGTACAAACTTGT 103

RESULT 38
AAC55465/C
ID AAC55465 standard; DNA; 204 BP.

XX
AC AAC55465;
AC AAC55465;
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST6 fragment nucleotide sequence #1.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
FN WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
FR 23-MAR-1999; 99US-0126049.
FR 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
DR
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX
XX Example 15; Fig 26; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX
SQ Sequence 204 BP; 70 A; 40 C; 46 G; 48 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 204;
Best Local Similarity 96.0%; Pred. No. 0.73;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
||||| ||||| ||||| ||||| |||||
Db 166 GTTCAGCTTTTGTACAAACTTGT 142

RESULT 39
AAC55470/C
ID AAC55470 standard; DNA; 204 BP.

XX
AC AAC55470;
AC AAC55470;
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST8 fragment nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
FN WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
FR 23-MAR-1999; 99US-0126049.
FR 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX
XX Example 15; Fig 28; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 125 BP; 61 A; 18 C; 14 G; 32 T; 0 other;

SQ Query Match 93.6%; Score 23.4; DB 21; Length 125;
Best Local Similarity 96.0%; Pred. No. 0.69; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||

DB 25 GTTCAGCTTTTGTACAACTTGT 1

RESULT 36
AAC55485/c
ID AAC55485 standard; DNA; 153 BP.

XX AAC55485;

AC AAC55485;

XX 11-JAN-2001 (first entry)

DT Destination vector pBEST15 fragment nucleotide sequence #2.

DE Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
mutant; recombinational cloning; entry vector; destination vector;
gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
OS Synthetic.

OS Synthetic.

PN WO200052027-A1.

XX 08-SEP-2000.

PD 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

PA Hartley JL, Brasch MA, Temple GF, Cheo D;
WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

XX Disclosure; Fig 35; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (i) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 153 BP; 52 A; 29 C; 33 G; 39 T; 0 other;

SQ Query Match 93.6%; Score 23.4; DB 21; Length 153;
Best Local Similarity 96.0%; Pred. No. 0.71; Mismatches 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||

DB 103 GTTCAGCTTTTGTACAACTTGT 79

RESULT 37
AAC55488/c
ID AAC55488 standard; DNA; 153 BP.

XX AAC55488;

AC AAC55488;

XX 11-JAN-2001 (first entry)

DT Destination vector pBEST16 fragment nucleotide sequence #2.

DE Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
mutant; recombinational cloning; entry vector; destination vector;
gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
OS Synthetic.

OS Synthetic.

PN WO200052027-A1.

XX 08-SEP-2000.

PD 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

PA Hartley JL, Brasch MA, Temple GF, Cheo D;
WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

XX Disclosure; Fig 36; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (i) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

XX
SQ
Sequence 102 BP: 37 A: 24 C: 19 G: 21 T: 1 other:
XX

Query Match	93.6%	Score 23.4	DB 21	Length 120
Best Local Similarity	96.0%	Pred. No.	0.69	
Matches 24	Conservative	0	Mismatches	1
		0	Indels	0
		0	Gaps	0

QY 1 GTTCAGCTTCTTGTACAAAATTGT 25
DB 118 GTTCAGCTTTTTTGTACAAAATTGT 94

RESULT 35
AAC55384/c
TD AAC55384 standard: DNA: 125 BP.

AAC55384;

11-JAN-2001 (first entry)

XX
DE
Recombination site nucleotide sequence attR1.

XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

XX Bacterionhage Lambda 05

XX
DN
WC3000E3037-A1

XX SEP 2000

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

PR 23-MAR-1999; 99US-0126049.

XX

XX
XX
-----XX
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533

DK
XX
NET, 2000-245240/45.

PT recombinational cloning of polypeptides - attL1, attL2, attR1, and attR2 nucleotide sequence useful for the isolated nucleic acid molecules encoding an attL1, attL2, attR1, attR2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

PS
xx
Claim 1; Fig 9; 459pp; English.

CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att

of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 40 A; 22 C; 18 G; 22 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.68;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
 |||||
 DB 83 GTTCAGCTTCTTGACAACTTGT 59

RESULT 32
 AAC55508/c
 ID AAC55508 standard; DNA; 102 BP.
 XX
 AC AAC55508;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST24 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 5; Fig 44; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (i) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 37 A; 25 C; 19 G; 21 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.68;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
 |||||
 DB 95 GTTCAGCTTCTTGACAACTTGT 71

RESULT 33
 AAC55511/c
 ID AAC55511 standard; DNA; 102 BP.
 XX
 AC AAC55511;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST25 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 5; Fig 45; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (i) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 XX SQ Sequence 102 BP; 35 A; 19 C; 20 G; 28 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.68;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 |||||
 Db 70 GTTCAGCTTTCTGTACAAACTTGT 46

RESULT 30
 AAC55500/c
 ID AAC55500 standard; DNA; 102 BP.
 XX
 AC AAC55500;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST21 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attL; attR;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW Gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 41; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 XX SQ Sequence 102 BP; 45 A; 13 C; 24 G; 20 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102;
 Best Local Similarity 96.0%; Pred. No. 0.68;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 |||||
 Db 82 GTTCAGCTTTCTGTACAAACTTGT 58

RESULT 31
 AAC55505/c
 ID AAC55505 standard; DNA; 102 BP.
 XX
 AC AAC55505;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST23 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attL; attR;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW Gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 5; Fig 43; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX Sequence 87 BP; 26 A; 19 C; 21 G; 21 T; 0 other;
SQ

Query Match 93.6%; Score 23.4; DB 21; Length 87;
Best Local Similarity 96.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
DB 79 GTTCAGCTTTCTGTACAACTTGT 55
|||||

RESULT 28
AAC55497/c
ID AAC55497 standard; DNA; 95 BP.
XX
AC AAC55497;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST20 fragment nucleotide sequence #2.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
XX Example 23; Fig 40; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX Sequence 95 BP; 41 A; 13 C; 15 G; 26 T; 0 other;
SQ

Query Match 93.6%; Score 23.4; DB 21; Length 95;
Best Local Similarity 96.0%; Pred. No. 0.68;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
DB 52 GTTCAGCTTTCTGTACAACTTGT 28
|||||

RESULT 29
AAC55458/c
ID AAC55458 standard; DNA; 102 BP.
XX
AC AAC55458;
XX
DT 11-JAN-2001 (first entry)
XX
DE GST expression cassette for destination vector pDEST3 #2.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Escherichia coli.
XX
PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
XX Example 15; Fig 23; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity

XX Example 7; Page 209; 357pp; English.
 XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination
 CC site nucleic acid sequences, and PCR primers of the invention. The
 CC att sequences are recognised by the recombination protein lambda
 CC integrase (Int). The invention is a new method of producing a population
 CC of hybrid nucleic acids comprising mixing at least a first population of
 CC nucleic acids comprising one or more recombination sites with at least
 CC one target nucleic acid comprising one or more recombination sites and
 CC causing some or all of the nucleic acids to recombine with all or some of
 CC the target nucleic acids. The method is useful for producing a population
 CC of hybrid nucleic acids which may be the same or different. The nucleic
 CC acids may be used to express therapeutic proteins or peptides and they
 CC may also be used to create novel fusion proteins by expressing different
 CC sequences linked to each other. The method allows simultaneous cloning of
 CC two or more different nucleic acids.
 XX Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;
 SQ

Query Match 93.6%; Score 23.4; DB 22; Length 43;
 Best Local Similarity 96.0%; Pred. No. 0.62; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 Db 29 GTTCAGCTTTCTGTACAAACTTGT 5

RESULT 26
 AAC5503/c
 ID AAC5503 standard; DNA; 82 BP.
 XX
 AC AAC5503;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST22 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 FN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 42: 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 82 BP; 39 A; 16 C; 17 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 21; Length 82;
 Best Local Similarity 96.0%; Pred. No. 0.67; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
 Db 70 GTTCAGCTTTCTGTACAAACTTGT 46

RESULT 27
 AAC5517/c
 ID AAC5517 standard; DNA; 87 BP.
 XX
 AC AAC5517;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST27 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 FN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 47: 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity

XX The invention relates to improving the production of a secondary
CC metabolite by a fungus. This involves modulating the expression of at
CC least one ZBC (zinc binuclear cluster protein) gene in a manner to
CC improve the yield of the secondary metabolite. Methods of the invention
CC may be used for improving the production of the secondary metabolite e.g.
CC antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such
CC as lovastatin or mevastatin), an immunosuppressant (such as cyclosporin A),
CC an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such
CC as avastin), a glucan synthase inhibitor, gliotoxin family of compounds,
CC a fungal toxin, a modulator of cell surface receptor signalling, a plant
CC growth regulator, a pigment, an insecticide, or an antineoplastic
CC compound. The method results in a decrease in fermentor run-time, a
CC decrease in the size of the fermentor required for the production of
CC equivalent amounts of the secondary metabolite, or a decrease in the
CC biomass required for the production, which translates into decreased
CC waste that must be handled in downstream processing. The sequences given
CC in records AB158597-AB158598 represent primers that are used in
CC construction of vectors containing the ZBC genes of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;
Query Match 93.6%; Score 23.4; DB 24; Length 35;
Best Local Similarity 96.0%; Pred. No. 0.61;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGACAACTTGT 25
DB 35 GTTCAGCTTTCTTGACAACTTGT 11
RESULT 24
AAC55545/c
ID AAC55545 standard; DNA; 43 BP.
XX
XX AAC55545;
DT 11-JAN-2001 (first entry)
XX
XX att site PCR primer attR1.
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; PCR primer; ss.
XX Bacteriophage lambda.
OS Synthetic.
OS
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
XX
XX 23-MAR-1999; 99US-0126049.
XX
XX 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides -
XX Example 19; Page 142; 459pp; English.
XX
XX

CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX
XX Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;
Query Match 93.6%; Score 23.4; DB 21; Length 43;
Best Local Similarity 96.0%; Pred. No. 0.62;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGACAACTTGT 25
DB 29 GTTCAGCTTTCTTGACAACTTGT 5
RESULT 25
AAS06217/c
ID AAS06217 standard; DNA; 43 BP.
XX
XX AAS06217;
XX
XX 12-SEP-2001 (first entry)
XX
XX PCR primer attR1 used to produce a population of hybrid DNA molecules.
XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
XX lambda integrase; therapeutic; ss.
XX Bacteriophage lambda.
OS Synthetic.
OS
XX WO200142509-A1.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US33546.
XX
XX 10-DEC-1999; 99US-0169983.
XX
XX 09-MAR-2000; 2000US-0188020.
XX
XX (CHEO/) CHEO D.
XX PA (BRAS/) BRASCH M A.
XX PA (TEMP/) TEMPLE G F.
XX PA (HART/) HARTLEY J L.
XX PA (BYRD/) BYRD D R N.
XX
XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one
XX or more recombination sites in the presence of recombination proteins,
XX e.g. Cre -
XX

PT nucleic acids -
 XX Disclosure; Page 262; 269pp; English.
 XX
 CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 25; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.59;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTTCTTGTACAAACTTGT 25
 Db 1 GTTCAGCTTTTGTACAAACTTGT 25
 RESULT 22
 AAH19591/c
 ID AAH19591 standard; DNA; 35 BP.
 XX
 AC AAH19591;
 XX
 DT 30-JUL-2001 (first entry)
 XX
 DE Plasmid pEZC7201 ccdB cassette PCR oligo MOS11.
 XX
 KW Secondary metabolite production; gene expression modulation;
 KW genetically modified fungus; antibacterial; antihypercholesterolaemic;
 KW immunosuppressant; cell surface receptor signalling; pigment;
 KW plant growth regulator; insecticide; anti-neoplastic; ccdB; death gene;
 KW pEZC7201; PCR primer; ss.
 XX
 OS Unidentified.
 XX
 XX WO200129073-A1.
 XX
 PD 26-APR-2001.
 XX
 XX 18-OCT-2000; 2000WO-US28903.
 XX
 XX 20-OCT-1999; 99US-0160587.
 XX
 XX 19-JAN-2000; 2000US-0487559.
 XX
 XX (MICR-) MICROBIA INC.
 XX
 XX Busby R, Doten R, Cali B, Hecht P, Holtzman D, Madden K, Maxon M;
 XX Milne T, Norman T, Rorer J, Salama S, Sherman A, Silva J;
 XX Summers E, Zhang L, Mayorga M, Feibelman T;
 XX
 XX WPI; 2001-374304/39.
 XX
 XX Improving production of secondary metabolite by fungus, for producing
 XX proteins of interest, involves modulating the expression of gene
 XX involved in regulation of secondary metabolite production -

XX
 PS
 XX
 XX Example 1; Page 67; 139pp; English.
 CC The present sequence is a primer which was used in an example
 CC illustrating an invention relating to a method for improving production
 CC of a secondary metabolite by a fungus. The method involves modulating
 CC the expression of a gene involved in the regulation of secondary
 CC metabolite production. The gene may be modulated in a manner that
 CC increases the yield or productivity of metabolite, increases
 CC efflux or excretion of the metabolite, decreases production of side
 CC effects or competing metabolites, alters the characteristics of the
 CC fungus in a manner that is beneficial to the production of the
 CC metabolite, causes conditional lysis of the fungus, or increases the
 CC resistance of the fungus to deleterious effects of exposure to the
 CC secondary metabolite. The method is useful for producing
 CC genetically modified fungi, which are useful for producing
 CC secondary metabolites such as antibacterial compounds,
 CC antihypercholesterolaemic compounds, immunosuppressants, modulators
 CC of cell surface receptor signalling, plant growth regulators, pigments,
 CC insecticides or anti-neoplastic compounds. The present sequence was
 CC used in the preparation of clones to regulate secondary metabolite
 CC production.
 XX
 SQ Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 22; Length 35;
 Best Local Similarity 96.0%; Pred. No. 0.61;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTTCTTGTACAAACTTGT 25
 Db 35 GTTCAGCTTTTGTACAAACTTGT 11
 RESULT 23
 ABL58593/c
 ID ABL58593 standard; DNA; 35 BP.
 XX
 AC ABL58593;
 XX
 DT 24-JUL-2002 (first entry)
 XX
 DE Oligonucleotide MOS11.
 XX
 KW Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein;
 KW antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastatin;
 KW mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine;
 KW angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin;
 KW fungal toxin; cell surface receptor; plant growth regulator; pigment;
 KW insecticide; antineoplastic; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 XX WO200224865-A2.
 XX
 XX 28-MAR-2002.
 XX
 XX 19-SEP-2001; 2001WO-US29288.
 XX
 XX 19-SEP-2000; 2000US-233564P.
 XX
 XX (MICR-) MICROBIA INC.
 XX
 XX Holtzman D, Madden K, Maxon M, Sherman A;
 XX
 XX WPI; 2002-352005/38.
 XX
 XX New method for improving the production of a secondary metabolite e.g.
 XX antineoplastic agent, ergot alkaloid from a fungus involves modulation
 XX of the expression of at least one zinc binuclear cluster protein gene
 XX -
 XX Example 1; SEQ ID 7; 49pp + sequence listing; English.

PF 30-MAY-2002; 2002WO-US17452.
XX
PR 30-MAY-2001; 2001US-294758P.
PR 21-MAR-2002; 2002US-366891P.
XX
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;
XX
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest -
XX
XX Claim 43; Page 143; 272pp; English.
PS
XX The present invention describes a eukaryotic chromosome (I) comprising
XX one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (1) a platform artificial chromosome
CC expression system (ACes) (II) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of ACes comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ
Query Match 93.6%; Score 23.4; DB 25; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25
RESULT 20
ABZ58734
ID ABZ58734 standard; DNA; 25 BP.
XX
AC ABZ58734;
XX
XX 01-MAY-2003 (first entry)
XX
XX Att site nucleotide sequence attR1.
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; att; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US15947.
XX
XX 21-MAY-2001; 2001US-291973P.
XX

PA (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
XX WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -
XX
XX Disclosure; Fig 13A; 273pp; English.
PS
XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
CC represent att recombination site sequences used in the method of the
CC invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ
Query Match 93.6%; Score 23.4; DB 25; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25
RESULT 21
ABT16628
ID ABT16628 standard; DNA; 25 BP.
XX
AC ABT16628;
XX
XX 03-APR-2003 (first entry)
XX
XX Artificial plant chromosome related oligo SEQ ID No 40.
DE
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX
XX Unidentified.
XX
XX WO200296923-A1.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US17451.
XX
XX 30-MAY-2001; 2001US-294687P.
PR 04-JUN-2001; 2001US-296329P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA (AGRI-) AGRISOMA INC.
XX
XX Perez C, Fabijanski SF, Perkins E;
XX
XX WPI; 2003-140436/13.
XX
XX Producing artificial chromosome by introducing a nucleic acid into
PT plant cell, selecting artificial chromosome that has one or more repeat
PT regions with equivalent amounts of euchromatic and heterochromatic

XX OS Bacteriophage lambda.
 XX PN WO200174861-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US10250.
 XX PR 31-MAR-2000; 2000US-193977P.
 XX PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 XX PI Vile RG, Harrington K, Murphy S, Bateman A;
 XX DR WPI; 2001-656985/75.
 XX PT Recombinant nucleic acid vector for reducing tumour size, has expression cassette comprising a promoter linked to nucleic acid sequence encoding a syncytium-inducing polypeptide and flanked on either side by recombinase -
 XX PS Disclosure; Page 42; 84pp; English.
 XX CC The invention relates to a recombinant nucleic acid vector comprising a first expression cassette, comprising a first promoter operably linked to a nucleic acid sequence encoding a syncytium-inducing polypeptide (such as a fusogenic membrane glycoprotein) and flanked on either side by a sequence recognised by a recombinase, and/or a second expression cassette comprising a tumour-specific promoter operably linked to a nucleic acid sequence encoding a recombinase. The nucleic acid of the first expression cassette may be linked to a hypoxic response element (HRE), the second expression cassette may contain a promoter linked to a nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to the nucleic acid encoding the recombinase. The tumour specific promoter is, for example, a carcinoembryonic antigen (CEA) promoter or a tyrosinase promoter and the recombinase is, for example, Cre recombinase or FLP recombinase. The invention is useful for reducing tumour size by administering the compositions as retroviral vectors, or in a cell containing the vector, to an individual in need of treatment for a disease caused by malignant cells. This sequence represents an Int recombinase site core region attnK2, required for excisive recombination.
 XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 10 T; 1 other;
 Query Match 93.6%; Score 23.4; DB 23; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.59;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTTGACAACTTGT 25
 Db 1 GTTCAGCTTCTTGACAACTTGT 25
 RESULT 18
 ID ABQ82121
 AC ABQ82121 standard; DNA; 25 BP.
 AC ABQ82121;
 XX DT 11-DEC-2002 (first entry)
 XX DE Core sequence of recombination site attR1 SEQ ID NO:4.
 XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
 KW recombination site; double stranded RNA; plant; ss.
 XX OS Synthetic.
 XX PN WO200259294-A1.
 XX PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-AU000073.
 XX 26-JAN-2001; 2001US-264067P.
 PR 29-NOV-2001; 2001US-333743P.
 XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX PI Wesley S, Waterhouse P, Helliwell C;
 XX DR WPI; 2002-682669/73.
 XX PT New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
 XX PS Disclosure; Page 14; 104pp; English.
 XX CC The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*;
 CC (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents the core sequence of recombination site attB1 which is given in the exemplification of the present invention.
 XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 24; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.59;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTTGACAACTTGT 25
 Db 1 GTTCAGCTTCTTGACAACTTGT 25
 RESULT 19
 ACC44658
 ID ACC44658 standard; DNA; 25 BP.
 XX AC ACC44658;
 XX DT 29-MAY-2003 (first entry)
 XX DE Recombination site related oligonucleotide SEQ ID NO:49.
 XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.
 XX OS Synthetic.
 XX PN WO200297059-A2.
 XX PD 05-DEC-2002.

Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 15
AAFS5743
ID AAF55743 standard; DNA; 25 BP.
XX
AC AAF55743;
XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attr1.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.
XX
PN US6171861-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JAN-1998; 98US-0005476.
XX
PR 07-JUN-1996; 96US-0663002.
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX
WPI; 2001-136877/14.
XX

In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host -
Claim 25; Column 46; 73pp; English.
The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector, to clone the nucleic acid. The present sequence is a recombination site, which may be used in the method of the present invention.

Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 16
AAC87874
ID AAC87874 standard; DNA; 25 BP.
XX
AC AAC87874;
XX
DT 02-MAR-2001 (first entry)
XX
DE Escherichia coli core region recombinant site attr1 SEQ ID NO:9.
XX

KW Core region; recombination site; cloning; chimeric DNA;
KW characteristic; mutation; att site; lox site; ss.
XX

OS Escherichia coli.

PN US6143557-A.

PD 07-NOV-2000.

PF 20-JAN-1999; 99US-0233493.

PR 07-JUN-1996; 96US-0663002.

PR 12-JAN-1998; 98US-0005476.

PR 07-JUN-1995; 95US-0486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered mutation -

Claim 1; Column 18; 73pp; English.

The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site or avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive.

Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 17
AAS14785
ID AAS14785 standard; DNA; 25 BP.
XX
AC AAS14785;
XX

27-FEB-2002 (first entry)

Lambda phage Int recombinase site core region DNA sequence attnR2.

Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine; syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour; tyrosinase; tumour-specific promoter; hypoxic response element; HRE; ss; tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer; cytostatic; gene therapy; Int recombinase site core region; attnR2; exclusive recombination.

CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that
CC have the desired characteristics and/or nucleic acid segments. The
CC methods can also be used for changing vectors. The oligonucleotides
CC AAX78935-X78994 are used in the method of the invention.

XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 20; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
DB 1 GTTCAGCTTTCTTGACAAACTTGT 25

RESULT 13

AAD14437
ID AAD14437 standard; DNA; 25 BP.

XX
AC AAD14437;

XX
DT 01-NOV-2001 (first entry)

XX
DE Recombination site attB3 DNA.

XX
KW Recombination site; copy number; replicon; recombinatorial cloning;
XX attB3; ds.

XX
OS Unidentified.

XX
PN US6270969-B1.

XX
PD 07-AUG-2001.

XX
PF 20-JAN-1999; 99US-0233492.

XX
PR 07-JUN-1996; 96US-0663002.

XX
PR 07-JUN-1995; 95US-0486139.

XX
PA (INVI-) INVITROGEN CORP.

XX
PI Hartley JL, Brasch MA;

XX
DR WPI; 2001-488248/53.

XX
PS Claim 14; Column 18; 76pp; English.
XX
Methods for apposing nucleic acids comprising an expression signal and
a gene/partial gene, using recombinatorial cloning by incubating the
nucleic acids in the presence of a recombination protein under
conditions for recombination -

XX
The invention relates to a method for apposing an expression signal and
a gene or partial gene, using recombinatorial cloning. The method
incubates nucleic acids comprising the expression signal and the gene/
partial gene in the presence of a recombination protein under conditions
sufficient to cause recombination and therefore appose the expression
signal and the gene or partial gene. The methods are useful for apposing
an expression signal and a gene or partial gene using recombinatorial
cloning. The methods are also useful for changing vectors, constructing
genes for fusion proteins, changing copy number, changing replicons,
cloning into phages, and cloning e.g., PCR products (with an attB site
at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
The methods are highly specific, rapid, and less labour intensive than
prior art methods. The present sequence is a recombination site
useful for recombination cloning.

XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
DB 1 GTTCAGCTTTCTTGACAAACTTGT 25

RESULT 14

AAS06181
ID AAS06181 standard; DNA; 25 BP.

XX
AC AAS06181;

XX
DT 12-SEP-2001 (first entry)

XX
DE Phage-lambda recombination site attR1.

XX
KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
XX lambda integrase; therapeutic; ss.

XX
OS Bacteriophage lambda.

XX
PN WO200142509-A1.

XX
PD 14-JUN-2001.

XX
PF 11-DEC-2000; 2000WO-US33546.

XX
PR 10-DEC-1999; 99US-0169983.

XX
PR 09-MAR-2000; 2000US-0188020.

XX
PA (CHEO/) CHEO D.

XX
PA (BRAS/) BRASCH M A.

XX
PA (TEMP/) TEMPLE G F.

XX
PA (HART/) HARTLEY J L.

XX
PA (BYRD/) BYRD D R N.

XX
PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX
DR WPI; 2001-356174/37.

XX
Producing hybrid nucleic acids, useful for expressing novel therapeutic
polypeptides, by mixing the same or different nucleic acids having one
or more recombination sites in the presence of recombination proteins,
e.g. Cre -

XX
PS Disclosure; Fig 24A; 357pp; English.

XX
AAS06174-AAS06322 represent Bacteriophage lambda att recombination
site nucleic acid sequences, and PCR primers of the invention. The
att sequences are recognised by the recombination protein lambda
integrase (Int). The invention is a new method of producing a population
of hybrid nucleic acids comprising mixing at least a first population of
nucleic acids comprising one or more recombination sites with at least
one target nucleic acid comprising one or more recombination sites and
causing some or all of the nucleic acids to recombine with all or some of
the target nucleic acids. The method is useful for producing a population
of hybrid nucleic acids which may be the same or different. The nucleic
acids may be used to express therapeutic proteins or peptides and they
may also be used to create novel fusion proteins by expressing different
sequences linked to each other. The method allows simultaneous cloning of
two or more different nucleic acids.

XX
SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25

```

XX 10-DEC-1999; 99US-0169983.
PR 09-MAR-2000; 2000US-0188020.
XX (CHEO/) CHEO D.
PA (BRAS/) BRASCH M A.
PA (TEMP/) TEMPLE G F.
PA (HART/) HARTLEY J L.
PA (BYRD/) BYRD D R N.
XX
XX Chao D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
FI WPI; 2001-356174/37.
XX
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
PT polypeptides, by mixing the same or different nucleic acids having one
PT or more recombination sites in the presence of recombination proteins,
PT e.g. Cre -
XX
XX Example 7; Page 209; 357pp; English.
XX
XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination
CC site nucleic acid sequences, and PCR primers of the invention. The
CC att sequences are recognised by the recombination protein lambda
CC integrase (Int). The invention is a new method of producing a population
CC of hybrid nucleic acids comprising mixing at least a first population of
CC nucleic acids comprising one or more recombination sites with at least
CC one target nucleic acid comprising one or more recombination sites and
CC causing some or all of the nucleic acids to recombine with all or some of
CC the target nucleic acids. The method is useful for producing a population
CC of hybrid nucleic acids which may be the same or different. The nucleic
CC acids may be used to express therapeutic proteins or peptides and they
CC may also be used to create novel fusion proteins by expressing different
CC sequences linked to each other. The method allows simultaneous cloning of
CC two or more different nucleic acids.
XX
XX Sequence 43 BP; 19 A; 5 C; 12 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 22; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 29 GTTCAGCTTTCTGTACAAACTTGT 5
XX
RESULT 11
AAT48218
ID AAT48218 standard; DNA; 25 BP.
XX
XX AAT48218;
XX
XX 20-OCT-1997 (first entry)
DT
DE attR1 core region.
XX
XX att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
XX Synthetic.
XX
XX WO9640724-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US100082.
XX
XX 07-JUN-1995; 95US-0486139.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Brasch MA, Hartley JL;
PI

```

```

XX WPI; 1997-065168/06.
XX
XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in
PT vitro or in vivo
XX
XX Claim 14; Page 55; 106pp; English.
XX
XX AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ
Query Match 93.6%; Score 23.4; DB 18; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.59;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25
XX
RESULT 12
AAX78943
ID AAX78943 standard; DNA; 25 BP.
XX
XX AAX78943;
XX
XX 17-AUG-1999 (first entry)
DT
XX Oligonucleotide #9 for recombination and cloning method.
DE
XX Cloning; donor; recombination site; vector; chimeric; ss.
KW
XX Synthetic.
OS
XX WO9921977-A1.
EN
XX 06-MAY-1999.
PD
XX
XX 26-OCT-1998; 98WO-US22589.
PF
XX
XX 23-OCT-1998; 98US-0177387.
PR
XX 24-OCT-1997; 97US-0065930.
PR
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Brasch MA, Fox DK, Hartley JL, Temple GF;
PI
XX WPI; 1999-303011/25.
XX
XX New nucleic acid cloning methods
PT
XX
XX Disclosure; Page 161; 185pp; English.
XX
XX The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more

```

PD 05-DEC-2002.
 XX 30-MAY-2002; 2002WO-US17451.
 PF 30-MAY-2001; 2001US-294687P.
 XX 04-JUN-2001; 2001US-296329P.
 PR (CHRO-) CHROMOSOMAL SYSTEMS INC.
 XX (AGRI-) AGRISOMA INC.
 PA Perez C, Fabijanski SF, Perkins E;
 XX WPI; 2003-140436/13.
 DR Producing artificial chromosome by introducing a nucleic acid into
 XX plant cell, selecting artificial chromosome that has one or more repeat
 PT regions with equivalent amounts of euchromatic and heterochromatic
 XX nucleic acids
 XX Disclosure; Page 262; 269pp; English.
 PS The invention relates to a novel method for producing plant artificial
 XX chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.
 XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTGT 25
 |||||
 Db 1 GTTCAGCTTTCTGTACAAACTGT 25

RESULT 9
 AAC55546/c
 ID AAC55546 standard; DNA; 43 BP.
 XX
 AC AAC55546;
 XX
 XX 11-JAN-2001 (first entry)
 DT
 XX att site PCR primer attR2.
 DE
 XX Bacteriophage lambda; att; recombination site; attB; attP; attL; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; PCR primer; ss.
 XX Bacteriophage lambda.
 OS Synthetic.
 OS WO200052027-A1.
 XX
 XX 08-SEP-2000.
 PD
 XX

PF 02-MAR-2000; 2000WO-US05432.
 XX 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX Example 19; Page 142; 459pp; English.
 PS The present invention describes isolated nucleic acid molecules (I)
 XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III) primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX Sequence 43 BP; 19 A; 5 C; 12 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTGT 25
 |||||
 Db 29 GTTCAGCTTTCTGTACAAACTGT 5

RESULT 10
 AAS06218/c
 ID AAS06218 standard; DNA; 43 BP.
 XX
 AC AAS06218;
 XX
 XX 12-SEP-2001 (first entry)
 DT
 XX PCR primer attR2 used to produce a population of hybrid DNA molecules.
 DE Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 XX lambda integrase; therapeutic; ss.
 KW Bacteriophage lambda.
 XX Synthetic.
 OS WO200142509-A1.
 XX
 XX 14-JUN-2001.
 XX
 XX 11-DEC-2000; 2000WO-US33546.
 PF

PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU00073.
XX
PR 26-JAN-2001; 2001US-264067P.
XX
PR 29-NOV-2001; 2001US-333743P.
XX
XX (CSR) COMMONWEALTH SCI & IND RES-ORG.
PA
PI Wesley S, Waterhouse P, Helliwell C;
XX
XX WPI; 2002-682669/73.
DR
XX
XX New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX
XX Disclosure; Page 14; 104pp; English.
PS
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerase of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
SQ

Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAACTTGT 25
DB 1 GTTCAGCTTCTGTGACAACTTGT 25

RESULT 7
ACC44659
ID ACC44659 standard; DNA; 25 BP.
XX
XX ACC44659;
AC
XX
DT 29-MAY-2003 (first entry)
XX
XX Recombination site related oligonucleotide SEQ ID NO:50.
DE
XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; PCR primer; ss.
XX
XX Synthetic.
OS
XX

PN WO200297059-A2.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-US17452.
XX
PR 30-MAY-2001; 2001US-294758P.
XX
PR 21-MAR-2002; 2002US-366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA
PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX Stewart S, Shellard J;
XX WPI; 2003-140461/13.
DR
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest -
XX
XX Claim 43; Page 143; 272pp; English.
PS
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (i) a platform artificial chromosome
CC expression system (ACes) (ii) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (ii) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (ii) by cell fusion, lipid-mediated transfection
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (ii) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of ACes comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
SQ

Query Match 100.0%; Score 25; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAACTTGT 25
DB 1 GTTCAGCTTCTGTGACAACTTGT 25

RESULT 8
ABT16629
ID ABT16629 standard; DNA; 25 BP.
XX
XX ABT16629;
AC
XX
DT 03-APR-2003 (first entry)
XX
XX Artificial plant chromosome related oligo SEQ ID NO 41.
DE
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
XX ds.
XX Unidentified.
OS
XX WO200296923-A1.
PN

Qy 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 4
AAF55744
ID AAF55744 standard; DNA; 25 BP.
XX
XX AAF55744;
XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attr2.
XX
XX Recombination site; cloning; att; ss.

OS Unidentified.
XX
XX US6171861-B1.
XX
XX 09-JAN-2001.
XX
XX 12-JAN-1998; 98US-0005476.
XX
XX 07-JUN-1996; 96US-0663002.
XX
XX 07-JUN-1995; 95US-0486139.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.

XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-136877/14.
XX
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host -
XX
XX Claim 25; Column 46; 73pp; English.

XX
XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule; and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention.

XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 5
AAC87875
ID AAC87875 standard; DNA; 25 BP.
XX
XX AAC87875;
XX
DT 02-MAR-2001 (first entry)
XX
XX Escherichia coli core region recombinant site attr2 SEQ ID NO:10.

XX
XX Core region; recombination site; cloning; chimeric DNA;
XX characteristic; mutation; att site; lox site; ss.
XX
XX Escherichia coli.

XX
XX US6143557-A.
XX
XX 07-NOV-2000.
XX
XX 20-JAN-1999; 99US-0233493.
XX
XX 07-JUN-1996; 96US-0663002.
XX
XX 12-JAN-1998; 98US-0005476.
XX
XX 07-JUN-1995; 95US-0486139.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.

XX
XX Brasch MA, Hartley JL;
XX
XX WPI; 2001-049004/06.

XX
XX Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation -

XX
XX Claim 1; Column 18; 73pp; English.

XX
XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the
CC above mentioned nucleic acids; and (4) cells comprising the above
CC mentioned nucleic acids or (IV). The nucleic acids are used in
CC engineering a core region of a given recombination site to provide
CC mutative sites suitable for subcloning reactions. The use of nucleic
CC acids for obtaining engineered recombination in vitro or in vivo makes
CC the methods for DNA or RNA subcloning, highly specific, rapid, and
CC less labour intensive.

XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 6
ABQ82122
ID ABQ82122 standard; DNA; 25 BP.
XX
XX ABQ82122;
XX
XX 11-DEC-2002 (first entry)

XX
XX Core sequence of recombination site attr2 SEQ ID NO:5.
XX
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ss.

XX
XX Synthetic.

PT vitro or in vivo
PS Claim 14; Page 55; 106pp; English.
XX
XX AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a CoIntegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTCTCTGTACAAACTTGT 25
RESULT 2
AXX78944
ID AAX78944 standard; DNA; 25 BP.
XX
XX AAX78944;
XX
XX 17-AUG-1999 (first entry)
XX
XX Oligonucleotide #10 for recombination and cloning method.
DE
XX
XX Cloning; donor; recombination site; vector; chimeric; ss.
KW
XX
XX Synthetic.
OS
XX
XX WO9921977-A1.
PN
XX
XX 06-MAY-1999.
PD
XX
XX 26-OCT-1998; 98WO-US22589.
PF
XX
XX 23-OCT-1998; 98US-0177387.
PR
XX
XX 24-OCT-1997; 97US-0065930.
PR
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX
XX Brasch MA, Fox DK, Hartley JL, Temple GF;
PI
XX
XX WPI; 1999-303011/25.
DR
XX
XX New nucleic acid cloning methods
PT
XX
XX Disclosure; Page 161; 185pp; English.
PS
XX
XX The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo; (1) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more
CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that

CC have the desired characteristics and/or nucleic acid segments. The
CC methods can also be used for changing vectors. The oligonucleotides
CC AAX78935-X78994 are used in the method of the invention.
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTCTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTCTCTGTACAAACTTGT 25
RESULT 3
AAD14438
ID AAD14438 standard; DNA; 25 BP.
XX
XX AAD14438;
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX Recombination site attR2 DNA.
DE
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
KW attR2; ds.
XX
XX Unidentified.
OS
XX
XX US6270969-B1.
FN
XX
XX 07-AUG-2001.
PD
XX
XX 20-JAN-1999; 99US-0233492.
PF
XX
XX 07-JUN-1996; 96US-0663002.
PR
XX
XX 07-JUN-1995; 95US-0486139.
PR
XX
XX (INVI-) INVITROGEN CORP.
PA
XX
XX Hartley JL, Brasch MA;
PI
XX
XX WPI; 2001-488248/53.
DR
XX
XX Methods for apposing nucleic acids comprising an expression signal and
PT a gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under
PT conditions for recombination -
XX
XX Claim 14; Column 18; 76pp; English.
PS
XX
XX The invention relates to a method for apposing an expression signal and
CC a gene or partial gene, using recombinatorial cloning. The method
CC incubates nucleic acids comprising the expression signal and the gene/
CC partial gene in the presence of a recombination protein under conditions
CC sufficient to cause recombination and therefore appose the expression
CC signal and the gene or partial gene. The methods are useful for apposing
CC an expression signal and a gene or partial gene using recombinatorial
CC cloning. The methods are also useful for changing vectors, constructing
CC genes for fusion proteins, changing copy number, changing replicons,
CC cloning into phages, and cloning e.g., PCR products (with an attB site
CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
CC The methods are highly specific, rapid, and less labour intensive than
CC prior art methods. The present sequence is a recombination site
CC useful for recombination cloning.
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:05:38 ; Search time 111.5 Seconds

(without alignments)
605.255 Million cell updates/sec

Title: US-10-055-001A-5

Perfect score: 25

Sequence: 1 gttcagctttctgtacaaactgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_19Jun03.*
1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	18	attR2 core region.
2	25	100.0	25	20	Oligonucleotide #1
3	25	100.0	25	22	Recombination site
4	25	100.0	25	22	Recombination site
5	25	100.0	25	22	Escherichia coli c
6	25	100.0	25	24	Core sequence of r
7	25	100.0	25	25	Recombination site
8	25	100.0	25	25	Artificial plant c

C	9	25	100.0	43	21	AAC55546	att site PCR prime
C	10	25	100.0	43	22	AAS06218	PCR primer attR2 u
	11	23.4	93.6	25	18	AAT48219	attR1 core region.
	12	23.4	93.6	25	20	AAI78943	Oligonucleotide #9
	13	23.4	93.6	25	22	AAI14437	Recombination site
	14	23.4	93.6	25	22	AAS06181	Phage-lambda recom
	15	23.4	93.6	25	22	AAF55743	Recombination site
	16	23.4	93.6	25	22	AAI87874	Escherichia coli c
	17	23.4	93.6	25	23	AAI14785	Lambda phage int x
	18	23.4	93.6	25	24	ABQ82121	Core sequence of r
	19	23.4	93.6	25	25	ACC44658	Recombination site
	20	23.4	93.6	25	25	ABZ58734	att site nucleotid
	21	23.4	93.6	25	25	ABT16628	Artificial plant c
C	22	23.4	93.6	35	22	AAH19591	Plasmid pZC7201 c
C	23	23.4	93.6	35	24	ABL58593	Oligonucleotide MO
C	24	23.4	93.6	43	21	AAC55545	att site PCR prime
C	25	23.4	93.6	43	22	AAI06217	PCR primer attR1 u
C	26	23.4	93.6	82	21	AAC55503	Destination vector
C	27	23.4	93.6	87	21	AAC55517	Destination vector
C	28	23.4	93.6	95	21	AAC55497	Destination vector
C	29	23.4	93.6	102	21	AAC55458	GST expression cas
C	30	23.4	93.6	102	21	AAC55500	Destination vector
C	31	23.4	93.6	102	21	AAC55505	Destination vector
C	32	23.4	93.6	102	21	AAC55508	Destination vector
C	33	23.4	93.6	102	21	AAC55511	Destination vector
C	34	23.4	93.6	120	21	AAC55453	Trc expression cas
C	35	23.4	93.6	125	21	AAC55384	Recombination site
C	36	23.4	93.6	153	21	AAC55485	Destination vector
C	37	23.4	93.6	153	21	AAC55488	Destination vector
C	38	23.4	93.6	204	21	AAC55465	Destination vector
C	39	23.4	93.6	204	21	AAC55470	Destination vector
C	40	23.4	93.6	204	21	AAC55476	Destination vector
C	41	23.4	93.6	255	21	AAC55460	Hisc-Trx expressio
C	42	23.4	93.6	255	21	AAC55478	Destination vector
C	43	23.4	93.6	306	21	AAC55468	Destination vector
C	44	23.4	93.6	306	21	AAC55514	Destination vector
C	45	23.4	93.6	420	21	AAC55492	Destination vector

ALIGNMENTS

RESULT 1
AAT48219
ID AAT48219 standard; DNA; 25 BP.
XX
AC AAT48219;
XX
DT 20-OCT-1997 (first entry)
DE
DE attR2 core region.
XX
XX
KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
OS Synthetic.
XX
XX WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US10082.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
DR WPI; 1997-065168/06.
XX
XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in


```
/note="pyruvate orthophosphate dikinase (pdk)"
/number=2
terminator 17922...18687
/note="octopine esynthase (ocs) terminator"
BASE COUNT 4837 a 4621 c 4607 g 4626 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 12; Length 18691;
Best Local Similarity 95.8%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAACTTG 24
|||||
Db 16418 GTTCAGCTTCTTGACAAAGTTG 16395
|||||

RESULT 38
AR124528 25 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 8 from patent US 6171861.
ACCESSION AR124528
VERSION AR124528.1 GI:14109889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 8 09-JAN-2001;
FEATURES
source
1. .25
/organism="unknown"
BASE COUNT 6 a 7 c 3 g 9 t
ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGACAAACTTGT 25
|||||
Db 4 CAGCTTCTTGACAAACTTGT 25

RESULT 39
AR163179 25 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 8 from patent US 6270969.
ACCESSION AR163179
VERSION AR163179.1 GI:16233687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 8 07-AUG-2001;
FEATURES
source
1. .25
/organism="unknown"
BASE COUNT 6 a 7 c 3 g 9 t
ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGACAAACTTGT 25
|||||
Db 4 CAGCTTCTTGACAAACTTGT 25

RESULT 40
AX491647 25 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 8 from Patent EPI227147.
ACCESSION AX491647
VERSION AX491647.1 GI:22324155
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 8 31-JUL-2002;
FEATURES
source
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 6 a 7 c 3 g 9 t
ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGACAAACTTGT 25
|||||
Db 4 CAGCTTCTTGACAAACTTGT 25

Search completed: November 6, 2003, 23:06:41
Job time : 601 secs
```



```

VERSION      BD131342.1  GI:23226287
KEYWORDS     JP 2002500861-A/16.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 25)
AUTHORS     Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE       Recombinational cloning using nucleic acids having recombination
JOURNAL     Patent: JP 2002500861-A 16 15-JAN-2002;
            LIFE TECHNOLOGIES INC
COMMENT      OS unknown
            PN JP 2002500861-A/16
            PD 15-JAN-2002
            PF 26-OCT-1998 JP 2000518069
            PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
            JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
            C12N15/09,C12Q1/68,C12N15/00
            CC Description of Unknown Organism: recombination products FH
            Key Location/Qualifiers
            FT source 1..25
            FT Location/Qualifiers
            FT /organism='Unknown'.
            FT Location/Qualifiers
            FT 1..25
            FT /organism='unidentified'
            FT /mol_type='genomic DNA'
            FT /db_xref='taxon:32644'
            FT 5 a 4 c 6 g 10 t

BASE COUNT  5 a 4 c 6 g 10 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTGTGACAACTTG 24
Db 1 GTTCAGCTTCTGTGACAACTTG 24

RESULT 36
CVE311874 18691 bp DNA circular SYN 09-JUL-2002
LOCUS      Cloning vector pHELLSGATE.
DEFINITION
ACCESSION  AJ311874
VERSION     AJ311874.1 GI:15982218
KEYWORDS   kanamycin resistance protein; neomycin phosphotransferase II; nptII
            gene; promoter; spec gene; spectinomycin resistance protein;
            transposon Tn7.
SOURCE     Cloning vector pHELLSGATE
ORGANISM   Cloning vector pHELLSGATE
            artificial sequences; vectors.
REFERENCE  1
AUTHORS     Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
            Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
            Gleave,A.P., Green,A.G. and Waterhouse,P.M.
            Construct design for efficient, effective and high-throughput gene
            silencing in plants
JOURNAL    Plant J. 27 (6), 581-590 (2001)
MEDLINE    21461301
PUBMED     11576441
REFERENCE  2 (bases 1 to 18691)
AUTHORS     Waterhouse,P.M.
TITLE      Direct Submission
JOURNAL    Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
            C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
FEATURES   Location/Qualifiers
            1..18691
            /organism="Cloning vector pHELLSGATE"
            /mol_type="genomic DNA"
            /db_xref="taxon:167049"
            /lab_host="Escherichia coli"
            /focus
            /notes="pHELLSGATE is a derivative of cloning vector
            PART27"

source
/organism="Escherichia coli K12"
/mol_type="genomic DNA"
/strain="K12"
/db_xref="taxon:83333"
265..448
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
449..1442
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
1443..7792
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
7793..9388
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
9389..11673
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
11674..13019
/organism="Cauliflower mosaic virus"
/mol_type="genomic DNA"
/db_xref="taxon:10641"
14660..16258
/organism="Flaveria trinervia"
/mol_type="genomic DNA"
/db_xref="taxon:4227"
17922..18691
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
264..447
/function="NOS promoter"
448..1269
/gene="nptII"
448..1269
/gene="nptII"
/note="neomycin phosphotransferase II (nptII)"
/codon_start=1
/transl_table=11
/product="kanomycin resistance protein"
/protein_id="CAC86252.1"
/db_xref="GI:15982219"
/db_xref="REMTREMBL:CAC86252"
/translacion="NAITLSATSLPISARIRAGSPAAWVERLFGYDWAQQTIGCSDA
VFRLSAQORPVLVKTDLSGALNELQDEARLSMLATTVCAAVLDVVTAGRDWLL
LGEVPGQDRLSHLAPAEKVSIMADMRHLTDPATCFPDQAKHRIERARTRMEAG
LVDDDLDEHQGLAPAEFLKARMPDGLVVTGDACLPIMVNGRFSGFIDC
GRIGWADRYQDIALATRDIAEELGCEWADRLVLYGIAAPDSQRTAFYRLDDEF"
1443..2148
/note="NOS terminator"
2149..2706
/note="left border"
7793..9388
/transposon="Tn7"
8600..9388
/gene="spec"
8600..9388
/gene="spec"
/codon_start=1
/transl_table=11
/product="spectinomycin resistance protein"
/protein_id="CAC86253.1"
/db_xref="GI:15982220"
/db_xref="REMTREMBL:CAC86253"
/translacion="MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSVDGGLKP
HSDIDLVTVTVRLEDTTFRALINDLLETSSAPGESEILRAVEVTIVVHDDIIPWRYP

```

```

BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24
|||||

RESULT 31
AX491650
LOCUS      25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 11 from Patent EP1227147.
ACCESSION AX491650
VERSION AX491650.1 GI:22324158
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE 1
AUTHORS      Hartley, J.L. and Brasch, M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1227147-A 11 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24
|||||

RESULT 32
AX491655
LOCUS      25 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 16 from Patent EP1227147.
ACCESSION AX491655
VERSION AX491655.1 GI:22324163
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE 1
AUTHORS      Hartley, J.L. and Brasch, M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1227147-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24
|||||

RESULT 33
AX498621
LOCUS      25 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 11 from Patent EP1229113.
ACCESSION AX498621
VERSION AX498621.1 GI:23343418
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE 1
AUTHORS      Hartley, J.L. and Brasch, M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1229113-A 11 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24
|||||

RESULT 34
AX498626
LOCUS      25 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 16 from Patent EP1229113.
ACCESSION AX498626
VERSION AX498626.1 GI:23343423
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE 1
AUTHORS      Hartley, J.L. and Brasch, M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1229113-A 16 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAAACTTG 24
|||||
Db 1 GTTCAGCTTCTTGTACAAAGTTG 24
|||||

RESULT 35
BD131342
LOCUS      25 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131342
```


Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db 3701 GTTCAGCTTTCTGTACAACTTGT 3725

RESULT 23
AX356862 13274 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 20 from Patent WO206490.
ACCESSION AX356862
VERSION AX356862.1 GI:18674110
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Dudler,R., Schaffrath,U. and Lawton,K.A.
TITLE Lipoxigenase genes, promoters, transit peptides and proteins thereof
JOURNAL Patent: WO 0206490-A 20 24-JAN-2002;
Syngenta Participations AG (CH) ; Universitaet Zuerich (CH)
FEATURES
source
1. .13274
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 3343 a 3271 c 3178 g 3482 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 13274;
Best Local Similarity 96.0%; Pred. No. 5;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db 4026 GTTCAGCTTTCTGTACAACTTGT 4050

RESULT 24
AF541939/c 13990 bp DNA linear SYN 01-DEC-2002
DEFINITION His-3 integration vector pJHAM007, complete sequence.
ACCESSION AF541939
VERSION AF541939.1 GI:25988997
KEYWORDS his-3 integration vector pJHAM007
SOURCE his-3 integration vector pJHAM007
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Description of a GATEWAY Destination Vector For High-Throughput Construction of Neurospora crassa Histidine-3 (his-3)-Gene Replacement Plasmids
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Biology, Texas A&M University, BSW #415, College Station, TX 77843-3258, USA
FEATURES
source
1. .13990
/organism="his-3 integration vector pJHAM007"
/mol_type="genomic DNA"
/specific_host="Neurospora crassa"
/db_xref="taxon:211505"
1. .3173
/note="pGEM132E(+)"
misc_feature 3174..8368
misc_feature /note="his-3 left flank; his-3 target integration site"
misc_feature 8430..8554

/note="attR1; Gateway; Bacteriophage Lambda recombination site"
8804..9463
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="AAN76304.1"
/db_xref="GI:25988998"
/translation="MEKKITGYTVVDISQMRKEHFEAFQSVQAQCTYNQVOLDITATF LKTVKNKHFPYPAFIHLARLMAHPEFRMAKDGELVIWDSVHPCTVFEHQPTFF SSLMEYHDDRFPLHIYSODVACVGENLAVFPKGFLENMFVSANPWSFTSFLNV ANMNFAPVFTMGKYYTQSGKVLMPALQVHHAVCDFGHVGRMLNELQQYCDVQGG A"
9805..10110
/note="ccdB"
/codon_start=1
/product="gyrase target toxin"
/protein_id="AAN76305.1"
/db_xref="GI:25988999"
/translation="MQFKVITYKRSRVRLFVDVQSDIIDTPGRMVIPLASARLLSD KVSRELYPVVHIGDESWMRTDMSVPVSVIGEEVADLSHRENDIKNAINDMFWGI"
misc_feature 10151..10275
/note="attR2; Gateway; Bacteriophage Lambda recombination site"
misc_feature 10419..13990
/note="his-3 right flank; his-3 target integration site"
BASE COUNT 3385 a 3549 c 3559 g 3497 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 13990;
Best Local Similarity 96.0%; Pred. No. 5;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db 8454 GTTCAGCTTTCTGTACAACTTGT 8430

RESULT 25
BD131368 25 bp DNA linear PAT 18-SEP-2002
LOCUS Recombinational cloning using nucleic acids having recombination sites.
DEFINITION BD131368
ACCESSION BD131368.1 GI:23226313
VERSION JP 2002500861-A/42.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination Patent: JP 2002500861-A 42 15-JAN-2002;
JOURNAL LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/42
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12N1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1..25
FT /organism='Unknown'.
FEATURES
source
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
4 a 3 c 9 t 6 others
BASE COUNT 4 a 3 c 9 t 6 others
ORIGIN
Query Match 90.4%; Score 22.6; DB 6; Length 25;

```

Db      1030 GTTCAGCTTTTGTACAACTTGT 1006
|||||
RESULT 20
AY196825      12677 bp      DNA      circular SYN 26-FEB-2003
LOCUS      PiggyBac transformation vector pB-UGIR w+, complete sequence.
DEFINITION
ACCESSION  AY196825
VERSION     AY196825.1  GI:28565731
KEYWORDS
SOURCE      piggyBac transformation vector pB-UGIR w+
ORGANISM    piggyBac transformation vector pB-UGIR w+
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 12677)
AUTHORS    Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL     Unpublished
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      Direct Submission
JOURNAL     Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES   Location/Qualifiers
            source          1..12677
                        /organism="piggyBac transformation vector pB-UGIR w+"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:221642"
                        complement(11..>620)
            repeat_region   632..998
                        /transposon="piggyBac transposable element"
            TATA_signal     632..998
                        /note="5x UAS hsp70 TATA signal"
            misc_feature    1003..2713
                        /note="Gateway recombination cassette A; attR1 Cmr ccdB
                        attR2"
            intron          2726..3040
                        /note="RpS5"
                        /number=3
            misc_feature    complement(3076..4788)
                        /note="Gateway recombination cassette B; attR1 Cmr ccdB
                        attR2"
            polyA_signal    4789..5246
                        /note="SV40"
            gene            5247..9369
                        /gene="w"
            repeat_region   complement(<9370..9819)
                        /transposon="piggyBac transposable element"
            misc_feature    3423 a 2924 c 2833 g 3497 t
                        /note="Gateway recombination cassette A; attR1 Cmr ccdB
                        attR2"
            intron          2726..3040
                        /note="RpS5"
                        /number=3
            misc_feature    complement(3076..4788)
                        /note="Gateway recombination cassette B; attR1 Cmr ccdB
                        attR2"
            polyA_signal    4789..5246
                        /note="SV40"
            gene            5247..9369
                        /gene="w"
            repeat_region   complement(<9370..9819)
                        /transposon="piggyBac transposable element"
            BASE COUNT      3423 a 2924 c 2833 g 3497 t
            ORIGIN
Query Match      93.6%; Score 23.4; DB 12; Length 12677;
Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db      1030 GTTCAGCTTTTGTACAACTTGT 1006
|||||
RESULT 22
AX590202      12789 bp      DNA      linear      PAT 24-JAN-2003
LOCUS      Sequence 9 from Patent WO02083888.
DEFINITION
ACCESSION  AX590202
VERSION     AX590202.1  GI:27901286
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Goossens,A. and Inz,D.
TITLE      The use of genes encoding membrane transporter pumps to stimulate
            the production of secondary metabolites in biological cells
JOURNAL     Patent: WO 02083888-A 9 24-OCT-2002;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
            Location/Qualifiers
            source          1..12789
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
                        /note="vector pK7MG2D"
            BASE COUNT      3050 a 3326 c 3397 g 3015 t
            ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 12789;

```

```

AUTHORS    Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 12677)
AUTHORS     Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE      Direct Submission
JOURNAL     Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES   Location/Qualifiers
            source          1..12677
                        /organism="piggyBac transformation vector pB-UGIR w+"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:221642"
                        complement(11..>620)
            repeat_region   632..998
                        /transposon="piggyBac transposable element"
            TATA_signal     632..998
                        /note="5x UAS hsp70 TATA signal"
            misc_feature    1003..2713
                        /note="Gateway recombination cassette A; attR1 Cmr ccdB
                        attR2"
            intron          2726..3040
                        /note="RpS5"
                        /number=3
            misc_feature    complement(3076..4788)
                        /note="Gateway recombination cassette B; attR1 Cmr ccdB
                        attR2"
            polyA_signal    4789..5246
                        /note="SV40"
            gene            5247..9369
                        /gene="w"
            repeat_region   complement(<9370..9819)
                        /transposon="piggyBac transposable element"
            BASE COUNT      3423 a 2924 c 2833 g 3497 t
            ORIGIN
Query Match      93.6%; Score 23.4; DB 12; Length 12677;
Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTCTGTACAACTTGT 25
|||||
Db      1030 GTTCAGCTTTTGTACAACTTGT 1006
|||||
RESULT 22
AX590202      12789 bp      DNA      linear      PAT 24-JAN-2003
LOCUS      Sequence 9 from Patent WO02083888.
DEFINITION
ACCESSION  AX590202
VERSION     AX590202.1  GI:27901286
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Goossens,A. and Inz,D.
TITLE      The use of genes encoding membrane transporter pumps to stimulate
            the production of secondary metabolites in biological cells
JOURNAL     Patent: WO 02083888-A 9 24-OCT-2002;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
            Location/Qualifiers
            source          1..12789
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
                        /note="vector pK7MG2D"
            BASE COUNT      3050 a 3326 c 3397 g 3015 t
            ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 12789;

```

```

CDS
/genes="ccdB"
complement(2241..2546)
/genes="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM622303.1"
/db_xref="GI:21552740"
/translation="MQPKVYTKRSRYRLVDVQSDIIDTPGRMVIPLASARLLSD
KYSRELPPVHHGDSEWRMTMDMASVPVSVIGSEVADLSHRENDIKNAINLFWGI"
complement(2888..3547)
/genes="CmR"
complement(2888..3547)
/genes="CmR"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="CmR"
/protein_id="AAM622302.1"
/db_xref="GI:21552739"
/translation="MEKKITGVTVDISOWHRKEHFAFQSVAAQCTVOTVOLDITPAF
LTKVKNKHVPAPFTHILARLMAHPEFARMKOGELVMDSVHPCTVFEHQETFE
SSLMSYHDDFQFLHIYSQDUNCYGENLAYFKGFIEFNFPVSANPWSFTSFDLNV
AMNDNFAPVFTMGKYYTGDKVLMLPLAIQVHHAVCDGPHVGRMLNELQQYCDQWQGG
A"
misc_feature
complement(3657..3783)
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 9019;
Best Local Similarity 96.0%; Pred. No. 5.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 25
|||||
Db 53 GTTCAGCTTCTTGTACAACTTGT 29

RESULT 18
AY196824
LOCUS piggyBac transformation vector pB-UGateway w+, complete sequence.
DEFINITION piggyBac transformation vector pB-UGateway w+
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS piggyBac transformation vector pB-UGateway w+
SOURCE piggyBac transformation vector pB-UGateway w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
source
1..11005
/organism="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..3620)
repeat_region
TATA_signal
643..999
/misc_feature
/notes="5x UAS hsp70 TATA signal"
1003..2713
attR2
intron
2726..3040
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
3574..7697
gene
/genes="w"
repeat_region
/notes="mini-white; derived from Drosophila"
complement(<7698..8147)
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 11005;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 25

```

```

intron
2726..3040
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
3574..7697
gene
/genes="w"
repeat_region
/notes="mini-white; derived from Drosophila"
complement(<7698..8147)
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 11005;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 25
|||||
Db 3089 GTTCAGCTTCTTGTACAACTTGT 3113

RESULT 19
AY196824/C
LOCUS piggyBac transformation vector pB-UGateway w+
DEFINITION piggyBac transformation vector pB-UGateway w+
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS piggyBac transformation vector pB-UGateway w+
SOURCE piggyBac transformation vector pB-UGateway w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
source
1..11005
/organism="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..3620)
repeat_region
TATA_signal
643..999
/misc_feature
/notes="5x UAS hsp70 TATA signal"
1003..2713
attR2
intron
2726..3040
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
3574..7697
gene
/genes="w"
repeat_region
/notes="mini-white; derived from Drosophila"
complement(<7698..8147)
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 12; Length 11005;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTACAACTTGT 25

```



```

/translation="MEKKITGYTTVDISQWHRKEHFEAFQSVQAQCTYNQTVOLDITAF
LKTVMKHKFYPAFHILARLMAHPEFRMAKDGELVINDSVHPCYTVFHEQTET
SSLSEYHDDRFQFLHIYSQDVACYGENLAYFPKGFLENMFVSANPWVSFTSFDLNV
ANMNDFFAPVFTMGKYITQGDVKVLMPLAIQVHHA VCDGPHVGRMLNELQYCDWQGG
A"
gene      1263..1568
          /gene="ccdB"
CDS       1263..1568
          /gene="ccdB"
          /note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
          /codon_start=1
          /product="CcdB"
          /protein_id="AAM62301.1"
          /db_xref="GI:21552738"
          /translation="MQFKVYTKRSRYRLFVDVQSDIIDTPGRMVIPLASARLLSD
KVSRELYPVVHIGDESRRMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
          1610..1736
misc_feature
          /note="attr2 of Gateway conversion cassette frame A"
          1762..2048
misc_feature
          /note="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
          complement(2073..3783)
repeat_region
          /note="antisense orientation of Gateway conversion
cassette frame A containing attr1-R2 repeats, Cmr gene and
ccdB gene"
          complement(2073..2199)
misc_feature
          /note="attr2 of Gateway conversion cassette frame A"
          complement(2241..2546)
gene
          /gene="ccdB"
          complement(2241..2546)
CDS
          /gene="ccdB"
          /note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
          /codon_start=1
          /product="CcdB"
          /protein_id="AAM62301.1"
          /db_xref="GI:21552740"
          /translation="MQFKVYTKRSRYRLFVDVQSDIIDTPGRMVIPLASARLLSD
KVSRELYPVVHIGDESRRMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
          complement(2888..3547)
gene
          /gene="Cmr"
          complement(2888..3547)
CDS
          /gene="Cmr"
          /function="confers resistance to antibiotic
chloramphenicol"
          /codon_start=1
          /product="Cmr"
          /protein_id="AAM62302.1"
          /db_xref="GI:21552739"
          /translation="MEKKITGYTTVDISQWHRKEHFEAFQSVQAQCTYNQTVOLDITAF
LKTVMKHKFYPAFHILARLMAHPEFRMAKDGELVINDSVHPCYTVFHEQTET
SSLSEYHDDRFQFLHIYSQDVACYGENLAYFPKGFLENMFVSANPWVSFTSFDLNV
ANMNDFFAPVFTMGKYITQGDVKVLMPLAIQVHHA VCDGPHVGRMLNELQYCDWQGG
A"
misc_feature
          complement(3657..3783)
          /note="attr1 of Gateway conversion cassette frame A"
          2337 a 2150 c 2185 g 2347 t
BASE COUNT
ORIGIN

Query Match      93.6%; Score 23.4; DB 12; Length 9019;
Best local Similarity 96.0%; Pred. No. 5.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTTCTTGTACAACTTGT 25
        |||||
Db      3756 GTTCAGCTTTTGTACAACTTGT 3780

RESULT 17
AF408413/c
LOCUS
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.

```

```

ACCESSION AF408413.1 GI:21552736
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 9019)
          BINARY vector pJawohl8-RNAi
          artificial sequences; vectors.
TITLE
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
JOURNAL pJawohl8-RNAi a binary vector for gene silencing in plants
REFERENCE 2 (bases 1 to 9019)
          Unpublished
          Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
          Direct Submission
          Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
          f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
          Germany
FEATURES
          Location/Qualifiers
          1..9019
             /organism="Binary vector pJawohl8-RNAi"
             /mol_type="genomic DNA"
             /db_xref="taxon:188084"
             /focus
             /note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
          3803..9019
             /organism="Binary vector pJawohl3-RNAi"
             /mol_type="genomic DNA"
             /db_xref="taxon:176105"
          26..1733
             /note="sense orientation of Gateway conversion cassette
frame A containing attr1-R2 repeats, Cmr gene and ccdB
gene"
          misc_feature
             26..152
             /note="attr1 of Gateway conversion cassette frame A"
          gene
             262..921
             /gene="Cmr"
          CDS
             262..921
             /gene="Cmr"
             /function="confers resistance to antibiotic
chloramphenicol"
             /codon_start=1
             /product="Cmr"
             /protein_id="AAM62300.1"
             /db_xref="GI:21552737"
             /translation="MEKKITGYTTVDISQWHRKEHFEAFQSVQAQCTYNQTVOLDITAF
LKTVMKHKFYPAFHILARLMAHPEFRMAKDGELVINDSVHPCYTVFHEQTET
SSLSEYHDDRFQFLHIYSQDVACYGENLAYFPKGFLENMFVSANPWVSFTSFDLNV
ANMNDFFAPVFTMGKYITQGDVKVLMPLAIQVHHA VCDGPHVGRMLNELQYCDWQGG
A"
          gene
             1263..1568
             /gene="ccdB"
          CDS
             1263..1568
             /gene="ccdB"
             /note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
             /codon_start=1
             /product="CcdB"
             /protein_id="AAM62301.1"
             /db_xref="GI:21552738"
             /translation="MQFKVYTKRSRYRLFVDVQSDIIDTPGRMVIPLASARLLSD
KVSRELYPVVHIGDESRRMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
             1610..1736
             /note="attr2 of Gateway conversion cassette frame A"
             1762..2048
             /note="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
             complement(2073..3783)
             /note="antisense orientation of Gateway conversion
cassette frame A containing attr1-R2 repeats, Cmr gene and
ccdB gene"
             complement(2073..2199)
             /note="attr2 of Gateway conversion cassette frame A"
             complement(2241..2546)
          gene

```

```

source
1. .4462
/organism="transfection vector pBtdest"
/mol_type="genomic DNA"
/db_xref="taxon:225975"
31. .443
/note="358"
421. .424
/note="358"
456. 580
/note="attR1"
689. .1348
/gene="cat"
689. .1348
/gene="cat"
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="CAD83080.1"
/db_xref="GI:29335743"
/translocation="MEXKITGYTVDISQWHRKEHFAPFOSVAQCTYNQTVQLDITAF
LKTWKYKHDFYPAFIIHLARLMAHPEFRMAKDGELVWDSVHPCYTFHEQETFF
SSLWSEYHDDPQFLHYSDVACYGENLAVFPKGFLENMFPVSANPWV3FTSFDLNV
ANMNDPAPVPTMGKYITQGDVLMPLAIQVHVAVCDFHVGRLNELQYCDSEWQGG
A"
1690. .1995
/gene="ccdB"
1690. .1995
/gene="ccdB"
/codon_start=1
/product="control of cell death B protein"
/protein_id="CAD83081.1"
/db_xref="GI:29335744"
/translocation="MQFKVYTYKRESRYLRFVDVQSDIIDTFGRRMVPIASARLLSD
KVSRLVPHVHIGDSWRMTTDMASVPVSIGVEADLSHRENDIKNAINLMPWGI"
2036. 2160
/note="attR2"
2168. .2463
/gene="nost"
2168. .2463
/gene="nost"
2606. 3466
/gene="amp"
2606. .3466
/gene="amp"
/codon_start=1
/product="beta lactamase"
/protein_id="CAD83082.1"
/db_xref="GI:29335745"
/translocation="MSIQHFRVALIPFAACLPVFAHPETLYKVKDAEDQLGARVGY
IELDLSGKILLESFRRFPMSTFKVLLCGAVLSRIDAGQEQQGRRIHYSQNDLVE
YSPVTEKHLDTGTVELCSAAITMSDNTAANLLTTIGPKELTAFLLNNQGDHVTPL
DRWPELNEATPNDERDTPMPVAMATTLRLITGLLTSLASRQQLIDWMEADKVAQPL
LRSLAPAGWFIADKSGAGERSGIIAALGPDGKPSRIWIYITGSGQATMDERNQIA
EIGASLIXHW"
BASE COUNT 1223 a 995 c 1065 g 1179 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 12; Length 4462;
Best Local Similarity 96.0%; Pred. No. 6.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
|||||
Db 480 GTTCAGCTTTCTTGACAAACTTGT 456

misc_feature
26. .152
/note="attR1 of Gateway conversion cassette frame A"
gene
262. .921
/gene="Cmr"
262. .921
/gene="Cmr"
CDS
262. .921
/gene="Cmr"
/function="confers resistance to antibiotic chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62300.1"
/db_xref="GI:21552737"

RESULT 15
AX306327/c
LOCUS
DEFINITION Sequence 10 from Patent WO0188121.
ACCESSION AX306327
VERSION AX306327.1 GI:17645566
KEYWORDS
SOURCE synthetic construct

```

```

ORGANISM synthetic construct
REFERENCE 1
AUTHORS Plaetinck,G., Renard,J.P. and Bogaert,T.
TITLE Vector constructs
JOURNAL Patent: WO 0188121-A 10 22-NOV-2001;
Devgen NV (BE)
FEATURES
source
1. .5148
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Plasmid pGN39"
BASE COUNT 1359 a 1199 c 1279 g 1311 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 5148;
Best Local Similarity 96.0%; Pred. No. 6;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAAACTTGT 25
|||||
Db 171 GTTCAGCTTTCTTGACAAACTTGT 147

RESULT 16
AF408413
LOCUS
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION AF408413
VERSION AF408413.1 GI:21552736
KEYWORDS
SOURCE
ORGANISM Binary vector pJawohl8-RNAi
Binary vector pJawohl8-RNAi
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE Direct Submision
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforchung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
source
1. .9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:188084"
/focus
/note="binary plant gene silencing vector for one-step cloning of inverted sequences"
3803. .9019
/organism="Binary vector pJawohl3-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26. .1733
/note="sense orientation of Gateway conversion cassette frame A containing attR1-R2 repeats, Cmr gene and ccdB gene"
26. .152
/note="attR1 of Gateway conversion cassette frame A"
gene
262. .921
/gene="Cmr"
262. .921
/gene="Cmr"
CDS
262. .921
/gene="Cmr"
/function="confers resistance to antibiotic chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62300.1"
/db_xref="GI:21552737"

```

```

/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
5 a 4 c 4 g 12 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 11
BD131335 25 bp DNA linear PAT 18-SEP-2002
LOCUS Recombinational cloning using nucleic acids having recombination
DEFINITION sites.
ACCESSION BD131335
VERSION JP 2002500861-A/9.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key source Location/Qualifiers
FT 1..25
/organism='Unknown'.
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
5 a 4 c 4 g 12 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 12
AX684690/c 35 bp DNA linear PAT 29-MAR-2003
LOCUS Sequence 9 from Patent WO0224865.
DEFINITION AX684690
ACCESSION AX684690.1 GI:29371240
VERSION
KEYWORDS Escherichia coli
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
TITLE Modulation of secondary metabolite production by zinc binuclear
Cluster proteins
Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
FEATURES
source
1..35
Location/Qualifiers
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
14 a 7 c 7 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 35;
Best Local Similarity 96.0%; Pred. No. 16;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 13
AX703501/c 1846 bp DNA linear PAT 03-APR-2003
LOCUS Sequence 63 from Patent WO0206653.
DEFINITION AX703501
ACCESSION AX703501.1 GI:29538461
VERSION
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Li,M. and Liu,Y.C.
TITLE Prokaryotic libraries and uses
JOURNAL Patent: WO 0206653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
source
1..1846
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
527 a 381 c 434 g 504 t
BASE COUNT
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 1846;
Best Local Similarity 96.0%; Pred. No. 7.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 25 GTTCAGCTTTTGTACAAACTTGT 1

RESULT 14
VFO551314/c 4462 bp DNA circular SYN 27-MAR-2003
LOCUS Transfection vector pBTdest.
DEFINITION AJ551314
ACCESSION AJ551314.1 GI:29335742
VERSION
KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
acetyl transferase; control of cell death B protein.
SOURCE Transfection vector pBTdest
ORGANISM Transfection vector pBTdest
REFERENCE 1
AUTHORS Jakoby,M.J., Heim,M.A. and Weisshaar,B.
TITLE Use of a gateway compatible vector for transient plant transfection
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4462)
AUTHORS Jakoby,M.J.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
FEATURES
Location/Qualifiers

```

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 6
AR124529
LOCUS AR124529 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6171861.
ACCESSION AR124529
VERSION AR124529.1 GI:14109890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 9 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..25
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 7
AR163180
LOCUS AR163180 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6270969.
ACCESSION AR163180
VERSION AR163180.1 GI:16233689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 9 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..25
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 8
AX269136
LOCUS AX269136 25 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 7 from Patent WO0174861.
ACCESSION AX269136
VERSION AX269136.1 GI:16542056
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
TITLE Compositions and methods for tissue specific gene regulation therapy
JOURNAL Patent: WO 0174861-A 7 11-OCT-2001;
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetically generated vector sequence"
BASE COUNT 5 a 5 c 4 g 10 t 1 others
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 9
AX491648
LOCUS AX491648 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 9 from Patent EP1227147.
ACCESSION AX491648
VERSION AX491648.1 GI:22324156
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 9 31-JUL-2002;
FEATURES Location/Qualifiers
source 1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 17;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAACTTGT 25

RESULT 10
AX498619
LOCUS AX498619 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 9 from Patent EP1229113.
ACCESSION AX498619
VERSION AX498619.1 GI:23343416
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 9 07-AUG-2002;
FEATURES Location/Qualifiers
source 1..25

```

source          1. .25
                /organism="unknown"
BASE COUNT      5 a      5 c      4 g      11 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAACTTGT 25
    |||
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 2
AX491649
LOCUS          25 bp      DNA
DEFINITION     Sequence 10 from patent US 6270969.
ACCESSION      AR163181
VERSION        AR163181
KEYWORDS       AR163181.1 GI:16233690
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 25)
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       Patent: US 6270969-A 10 07-AUG-2001;
FEATURES      Location/Qualifiers
                source
                1. .25
                /organism="unknown"
                /db_xref="taxon:32644"
BASE COUNT     5 a      5 c      4 g      11 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAACTTGT 25
    |||
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 3
AX491649
LOCUS          25 bp      DNA
DEFINITION     Sequence 10 from Patent EP1227147.
ACCESSION      AX491649
VERSION        AX491649.1 GI:22324157
KEYWORDS
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       Patent: EP 1227147-A 10 31-JUL-2002;
FEATURES      Location/Qualifiers
                source
                1. .25
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
BASE COUNT     5 a      5 c      4 g      11 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAACTTGT 25
    |||
Db 1 GTTCAGCTTCTTGACAACTTGT 25

source          1. .25
                /organism="unknown"
BASE COUNT      5 a      5 c      4 g      11 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAACTTGT 25
    |||
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 4
AX498620
LOCUS          25 bp      DNA
DEFINITION     Sequence 10 from Patent EP1229113.
ACCESSION      AX498620
VERSION        AX498620.1 GI:23343417
KEYWORDS
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       Patent: EP 1229113-A 10 07-AUG-2002;
FEATURES      Location/Qualifiers
                source
                1. .25
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
BASE COUNT     5 a      5 c      4 g      11 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAACTTGT 25
    |||
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 5
BD131336
LOCUS          25 bp      DNA
DEFINITION     Recombinational cloning using nucleic acids having recombination
                sites.
ACCESSION      BD131336
VERSION        BD131336.1 GI:23226281
KEYWORDS       JP 2002500861-A/10.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 25)
AUTHORS       Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE         Recombinational cloning using nucleic acids having recombination
JOURNAL       Patent: JP 2002500861-A 10 15-JAN-2002;
COMMENT       LIFE TECHNOLOGIES INC
                OS Unknown
                PN JP 2002500861-A/10
                PD 15-JAN-2002
                PF 26-OCT-1998 JP 2000518069
                PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
                CI2N15/09, CI2Q1/68, CI2N15/00
                CC Description of Unknown Organism: recombination products PH
                Key
                Location/Qualifiers
                FT source
                1. .25
                /organism="Unknown".
                FT Location/Qualifiers
                1. .25
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
BASE COUNT     5 a      5 c      4 g      11 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAACTTGT 25
    |||
Db 1 GTTCAGCTTCTTGACAACTTGT 25

```

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-5
Perfect score: 25
Sequence: 1 gttcagctttcttgracaacttgt 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_on.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pin.*
35: em_htg_rod.*
36: em_htg_man.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	25	100.0	25	6	AR124530	AR124530 Sequence
2	25	100.0	25	6	AR163181	AR163181 Sequence
3	25	100.0	25	6	AX491649	AX491649 Sequence
4	25	100.0	25	6	AX498620	AX498620 Sequence
5	25	100.0	25	6	BD131336	BD131336 Recombina
6	23.4	93.6	25	6	AR124529	AR124529 Sequence
7	23.4	93.6	25	6	AR163180	AR163180 Sequence
8	23.4	93.6	25	6	AX269136	AX269136 Sequence
9	23.4	93.6	25	6	AX491648	AX491648 Sequence
10	23.4	93.6	25	6	AX498619	AX498619 Sequence
11	23.4	93.6	25	6	BD131335	BD131335 Recombina
12	23.4	93.6	35	6	AX684690	AX684690 Sequence
13	23.4	93.6	1846	6	AX703501	AX703501 Sequence
14	23.4	93.6	4462	12	VFO551314	AJ551314 Transfect
15	23.4	93.6	5148	6	AX306327	AX306327 Sequence
16	23.4	93.6	9019	12	AF408413	AF408413 Binary ve
17	23.4	93.6	9019	12	AY196824	AY196824 PiggyBac
18	23.4	93.6	11005	12	AY196824	AY196824 PiggyBac
19	23.4	93.6	11005	12	AY196825	AY196825 PiggyBac
20	23.4	93.6	12677	12	AY196825	AY196825 PiggyBac
21	23.4	93.6	12677	12	AY196825	AY196825 PiggyBac
22	23.4	93.6	12789	6	AX590202	AX590202 Sequence
23	23.4	93.6	13274	6	AX356862	AX356862 Sequence
24	23.4	93.6	13990	12	AF541939	AF541939 His-3 int
25	22.6	90.4	25	6	BD131368	BD131368 Recombina
26	22.4	89.6	25	6	AR124531	AR124531 Sequence
27	22.4	89.6	25	6	AR124536	AR124536 Sequence
28	22.4	89.6	25	6	AR163182	AR163182 Sequence
29	22.4	89.6	25	6	AR163187	AR163187 Sequence
30	22.4	89.6	25	6	AX269137	AX269137 Sequence
31	22.4	89.6	25	6	AX491650	AX491650 Sequence
32	22.4	89.6	25	6	AX491655	AX491655 Sequence
33	22.4	89.6	25	6	AX498621	AX498621 Sequence
34	22.4	89.6	25	6	AX498626	AX498626 Sequence
35	22.4	89.6	25	6	BD131342	BD131342 Recombina
36	22.4	89.6	18691	12	CVE311874	AJ311874 Cloning v
37	22.4	89.6	18691	12	CVE311874	AJ311874 Cloning v
38	22.4	88.0	25	6	AR124528	AR124528 Sequence
39	22.4	88.0	25	6	AR163179	AR163179 Sequence
40	22.4	88.0	25	6	AX491647	AX491647 Sequence
41	22.4	88.0	25	6	AX498618	AX498618 Sequence
42	21.8	87.2	25	6	BD131337	BD131337 Recombina
43	21.8	87.2	1846	6	AX703501	AX703501 Sequence
44	21.8	87.2	4462	12	VFO551314	AJ551314 Transfect
45	21.8	87.2	5148	6	AX306327	AX306327 Sequence

ALIGNMENTS

RESULT 1	AR124530	Sequence 10 from patent US 6171861.	25 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	AR124530	Sequence 10 from patent US 6171861.				
DEFINITION	AR124530	Sequence 10 from patent US 6171861.				
ACCESSION	AR124530	Sequence 10 from patent US 6171861.				
VERSION	AR124530.1	GI:14109891				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Hartley,J.L. and Brasch,M.A.					
TITLE	Recombinational cloning using engineered recombination sites					
JOURNAL	Patent: US 6171861-A 10 09-JAN-2001;					
FEATURES	Location/Qualifiers					

```
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 13050 GTTCAGCTTCTTGACAAACTTGT 13026

RESULT 38
US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 93.6%; Score 23.4; DB 14; Length 17681;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 16879 GTTCAGCTTCTTGACAAACTTGT 16903

RESULT 39
US-10-055-001A-26/c
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 93.6%; Score 23.4; DB 14; Length 17681;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 13050 GTTCAGCTTCTTGACAAACTTGT 13026

RESULT 40
```

```
US-09-855-797A-42
; Sequence 42, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942,2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-42

Query Match 90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 1 GTTCAGCTTCTTGACAAACTTGT 25

Search completed: November 7, 2003, 02:22:26
Job time : 103.25 secs
```

```
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match          93.6%; Score 23.4; DB 14; Length 17458;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 34
US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match          93.6%; Score 23.4; DB 12; Length 17476;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
Db 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 35
US-10-385-546-7/c
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match          93.6%; Score 23.4; DB 12; Length 17476;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 36
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match          93.6%; Score 23.4; DB 14; Length 17476;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAACTTGT 25
Db 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 37
US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match          93.6%; Score 23.4; DB 14; Length 17476;
```



```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 6464
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDEST1
; FEATURE:
; NAME/KEY: gene
; LOCATION: (216)..(257)
; OTHER INFORMATION: T7c promoter
; FEATURE:
; NAME/KEY: gene
; LOCATION: (273)..(393)
; OTHER INFORMATION: attR1
; FEATURE:
; NAME/KEY: gene
; LOCATION: (647)..(1306)
; OTHER INFORMATION: Cmr
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1426)..(1510)
; OTHER INFORMATION: inactivated ccdA
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1648)..(1953)
; OTHER INFORMATION: ccdB
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1994)..(2118)
; OTHER INFORMATION: attR2
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2598)..(3503)
; OTHER INFORMATION: ampR
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4104)..(4264)
; OTHER INFORMATION: ori
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4504)..(4941)
; OTHER INFORMATION: flori (f1 intergenic region)
; FEATURE:
; NAME/KEY: gene
; LOCATION: (5340)..(6420)
; OTHER INFORMATION: lacIq
; US-10-151-690-20
;
; Query Match 93.6%; Score 23.4; DB 14; Length 6464;
; Best Local Similarity 96.0%; Pred. No. 1.2;
; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
; Db 297 GTTCAGCTTTTGTACAAACTTGT 273
;
; RESULT 31
; US-09-887-576-581/c
; Sequence 581, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
;
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 581
; LENGTH: 11180
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-887-576-581
;
; Query Match 93.6%; Score 23.4; DB 10; Length 11180;
; Best Local Similarity 96.0%; Pred. No. 1.3;
; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
; Db 142 GTTCAGCTTTTGTACAAACTTGT 118
;
; RESULT 32
; US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
; US-10-055-001A-25
;
; Query Match 93.6%; Score 23.4; DB 14; Length 17458;
; Best Local Similarity 96.0%; Pred. No. 1.4;
; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
; Db 16656 GTTCAGCTTTTGTACAAACTTGT 16680
;
; RESULT 33
; US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
```

; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; TYPE: DNA
; ORGANISM: attR1 PCR Primer
US-09-732-914-44

Query Match 93.6%; Score 23.4; DB 9; Length 43;
Best Local Similarity 96.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||||
Db 29 GTTCAGCTTTTGTACAAACTTGT 5

RESULT 27
US-10-151-690-19/c
; Sequence 19, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDEST1
US-10-151-690-19

Query Match 93.6%; Score 23.4; DB 14; Length 120;
Best Local Similarity 96.0%; Pred. No. 0.62;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||||
Db 118 GTTCAGCTTTTGTACAAACTTGT 94

RESULT 28
US-10-023-208-63/c
; Sequence 63, Application US/10023208
; Publication No. US20030124537A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; APPLICANT: Liu, Yuan-Ching
; TITLE OF INVENTION: PROKARYOTIC LIBRARIES AND USES
; FILE REFERENCE: A-70174-1/RET/RMS/RMK

; CURRENT APPLICATION NUMBER: US/10/023,208
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,163
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-023-208-63

Query Match 93.6%; Score 23.4; DB 14; Length 1846;
Best Local Similarity 96.0%; Pred. No. 0.98;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||||
Db 25 GTTCAGCTTTTGTACAAACTTGT 1

RESULT 29
US-10-241-596-137/c
; Sequence 137, Application US/10241596
; Publication No. US20030166238A1
; GENERAL INFORMATION:
; APPLICANT: Microbiological Research Authority
; APPLICANT: The Speywood Laboratory Limited
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130003
; CURRENT APPLICATION NUMBER: US/10/241,596
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: US 09/242,689
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB 9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB 9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 5558
; TYPE: DNA
; ORGANISM: Clostridium botulinum
US-10-241-596-137

Query Match 93.6%; Score 23.4; DB 12; Length 5558;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
|||||
Db 1666 GTTCAGCTTTTGTACAAACTTGT 1642

RESULT 30
US-10-151-690-20/c
; Sequence 20, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.

APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-162-879-9

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAACTTGT 25
|||||
Db 1 GTTCAGCTTCTTGTACAACTTGT 25

RESULT 23
US-10-161-403-49
; Sequence 49, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attr1
US-10-161-403-49

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAACTTGT 25
|||||
Db 1 GTTCAGCTTCTTGTACAACTTGT 25

RESULT 24
US-10-151-690-32
; Sequence 32, Application US/10151690

Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr1
US-10-151-690-32

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAACTTGT 25
|||||
Db 1 GTTCAGCTTCTTGTACAACTTGT 25

RESULT 25
US-09-974-760B-33/c
; Sequence 33, Application US/09974760B
; Publication No. US20030143705A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Shannon
; APPLICANT: Sherman, Amir
; APPLICANT: Trueheart, Joshua
; APPLICANT: Milne, G. Todd
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES
; FILE REFERENCE: 14184-009001
; CURRENT APPLICATION NUMBER: US/09/974,760B
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-974-760B-33

Query Match 93.6%; Score 23.4; DB 12; Length 35;
Best Local Similarity 96.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAACTTGT 25
|||||
Db 35 GTTCAGCTTCTTGTACAACTTGT 11

RESULT 26
US-09-732-914-44/c
; Sequence 44, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.

```
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-10-300-892-9

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 20
US-10-055-001A-4
; Sequence 4, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attr1
; US-10-055-001A-4

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 21
US-10-058-292-9
; Sequence 9, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
```

```
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-Jan-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-Jan-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-Jun-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-Jun-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-058-292-9

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 22
US-10-162-879-9
; Sequence 9, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
```

```

; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-907-719-9

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTTGTCACAAACTGT 25
        |||||
DB      1 GTTCAGCTTTTGTGTCACAAACTGT 25

RESULT 17
US-09-432-085-9
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/432,085
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-985-448-9

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTTGTCACAAACTGT 25
        |||||
DB      1 GTTCAGCTTTTGTGTCACAAACTGT 25

RESULT 18
US-09-985-448-9
; Sequence 9, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-985-448-9

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTTGTCACAAACTGT 25
        |||||
DB      1 GTTCAGCTTTTGTGTCACAAACTGT 25

RESULT 19
US-10-300-892-9
; Sequence 9, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004

```

```

; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: Recombination Sites
; CURRENT APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-9

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches      24; Conservative    0; Mismatches   1; Indels     0; Gaps      0;

QY      1 GTTCAGCTTCTTGACAAACTGT 25
Db       | ||||| ||||||| ||||||| |||||
        1 GTTCAGCTTTTGTACAAACTGT 25

RESULT 17
US-09-432-085-9
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/563,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139

```

```

; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-9

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTTGACAAACTGT 25
        |||||
DB       1 GTTCAGCTTTTGTACAAACTGT 25

RESULT 17
US-09-432-085-9
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/432,085
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-9

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTTGACAAACTGT 25
        |||||
DB       1 GTTCAGCTTTTGTACAAACTGT 25

RESULT 18
US-09-985-448-9
; Sequence 9, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-9

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.47;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCTTGACAAACTGT 25
        |||||
DB       1 GTTCAGCTTTTGTACAAACTGT 25

RESULT 19
US-10-300-892-9
; Sequence 9, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; RECOMBINATION SITES
; FILE REFERENCE: 0942.2850004

```

Sequence 8, Application US/09732914
 Patent No. US20020007051A1
 GENERAL INFORMATION:
 APPLICANT: Cheo, David
 APPLICANT: Brasch, Michael A.
 APPLICANT: Temple, Gary F.
 APPLICANT: Hartley, James L.
 APPLICANT: Byrd, Devon R.N.
 TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
 TITLE OF INVENTION: Recombinational Cloning
 FILE REFERENCE: 0942.5010002
 CURRENT APPLICATION NUMBER: US/09/732,914
 CURRENT FILING DATE: 2000-12-11
 PRIOR APPLICATION NUMBER: US 60/169,983
 PRIOR FILING DATE: 1999-12-10
 PRIOR APPLICATION NUMBER: US 60/188,020
 PRIOR FILING DATE: 2000-03-09
 NUMBER OF SEQ ID NOS: 140
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 8
 LENGTH: 25
 TYPE: DNA
 ORGANISM: attr1
 US-09-732-914-8

Query Match 93.6%; Score 23.4; DB 9; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.47; 1; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
 DB 1 GTTCAGCTTTCTTGACAACTTGT 25

RESULT 13
 US-09-855-797A-9
 Sequence 9, Application US/09855797A
 Patent No. US2002009457A1
 GENERAL INFORMATION:
 APPLICANT: Hartley, James L.
 APPLICANT: Brasch, Michael A.
 APPLICANT: Temple, Gary F.
 APPLICANT: Fox, Donna K.
 TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 TITLE OF INVENTION: Recombination Sites
 FILE REFERENCE: 0942.2850008
 CURRENT APPLICATION NUMBER: US/09/855,797A
 CURRENT FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: 09/296,281
 PRIOR FILING DATE: 1999-04-22
 PRIOR APPLICATION NUMBER: US 60/065,930
 PRIOR FILING DATE: 1997-10-24
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 9
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: recombination
 OTHER INFORMATION: products
 US-09-855-797A-9

Query Match 93.6%; Score 23.4; DB 9; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.47; 1; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
 DB 1 GTTCAGCTTTCTTGACAACTTGT 25

RESULT 14

US-09-822-634-7
 Sequence 7, Application US/09822634
 Patent No. US2002015056A1
 GENERAL INFORMATION:
 APPLICANT: Vile, Richard G.
 APPLICANT: Harrington, Kevin
 APPLICANT: Bateman, Andrew
 APPLICANT: Murphy, Steven
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
 TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
 FILE REFERENCE: 07039-289001
 CURRENT APPLICATION NUMBER: US/09/822,634
 CURRENT FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: 60/193,977
 PRIOR FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetically generated vector sequence
 US-09-822-634-7

Query Match 93.6%; Score 23.4; DB 10; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.47; 1; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
 DB 1 GTTCAGCTTTCTTGACAACTTGT 25

RESULT 15
 US-09-907-900-9
 Sequence 9, Application US/09907900
 Patent No. US20020172997A1
 GENERAL INFORMATION:
 APPLICANT: Hartley, James L.
 APPLICANT: Brasch, Michael A.
 APPLICANT: Temple, Gary F.
 APPLICANT: Fox, Donna K.
 TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 TITLE OF INVENTION: Recombination Sites
 FILE REFERENCE: 0942.2850004
 CURRENT APPLICATION NUMBER: US/09/907,900
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: 09/177,387
 PRIOR FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 9
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: recombination
 OTHER INFORMATION: products
 US-09-907-900-9

Query Match 93.6%; Score 23.4; DB 10; Length 25;
 Best Local Similarity 96.0%; Pred. No. 0.47; 1; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGACAACTTGT 25
 DB 1 GTTCAGCTTTCTTGACAACTTGT 25

RESULT 16
 US-09-907-719-9
 Sequence 9, Application US/09907719

Fri Nov 7 08:08:40 2003

us-10-055-001a-5.rnpb

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
DB 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 9
US-10-162-879-10
; Sequence 10, Application US/10162879
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-162-879-10

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
DB 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 10
US-10-161-403-50
; Sequence 50, Application US/10161403
; Publication No. US2003011910A1
; GENERAL INFORMATION:

APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: attr2
US-10-161-403-50

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
DB 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 11
US-09-732-914-45/c
; Sequence 45, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 43
; TYPE: DNA
; ORGANISM: attr2 PCR Primer
US-09-732-914-45

Query Match 100.0%; Score 25; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
DB 29 GTTCAGCTTCTTGACAACTTGT 5

RESULT 12
US-09-732-914-8

QY	1	GTTCAGCTTTCTTGTACAAACTTGT	25
pb	1	GTTCAGCTTTCTTGTACAAACTTGT	25

FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2500

APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs

us-10-055-001a-5.rnpb

Fri Nov 7 08:08:40 2003

```

US-09-907-900-10
; Sequence 10, Application US/09907900
; Publication No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-10

Query Match      100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 3
US-09-907-719-10
; Sequence 10, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-10

Query Match      100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 4
US-09-432-085-10
; Sequence 10, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-10

Query Match      100.0%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAACTTGT 25
Db 1 GTTCAGCTTCTTGACAACTTGT 25

RESULT 5
US-09-985-448-10
; Sequence 10, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 23:06:49 ; Search time 102.25 Seconds
(without alignments)
780.185 Million cell updates/sec

Title: US-10-055-001A-5

Perfect score: 25

Sequence: 1 gttcagctttctgtacaaactgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2141354 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	25	100.0	25	9	US-09-855-797A-10
2	25	100.0	25	10	US-09-907-900-10
3	25	100.0	25	10	US-09-907-719-10
4	25	100.0	25	11	US-09-432-085-10
5	25	100.0	25	12	US-09-985-448-10
6	25	100.0	25	12	US-10-300-892-10
7	25	100.0	25	14	US-10-055-001A-5
8	25	100.0	25	14	US-10-058-292-10
9	25	100.0	25	14	US-10-162-879-10
10	25	100.0	25	14	US-10-161-403-50
11	25	100.0	43	9	US-09-732-914-45
12	23.4	93.6	25	9	US-09-732-914-8
13	23.4	93.6	25	9	US-09-855-797A-9
14	23.4	93.6	25	10	US-09-822-634-7
15	23.4	93.6	25	10	US-09-907-900-9
16	23.4	93.6	25	10	US-09-907-719-9

17	23.4	93.6	25	11	US-09-432-085-9	Sequence 9, Appli
18	23.4	93.6	25	12	US-09-985-448-9	Sequence 9, Appli
19	23.4	93.6	25	12	US-10-300-892-9	Sequence 9, Appli
20	23.4	93.6	25	14	US-10-055-001A-4	Sequence 4, Appli
21	23.4	93.6	25	14	US-10-058-292-9	Sequence 9, Appli
22	23.4	93.6	25	14	US-10-162-879-9	Sequence 9, Appli
23	23.4	93.6	25	14	US-10-161-403-49	Sequence 49, Appli
24	23.4	93.6	25	14	US-10-151-690-32	Sequence 32, Appli
25	23.4	93.6	25	12	US-09-974-760B-33	Sequence 33, Appli
26	23.4	93.6	35	12	US-09-732-914-44	Sequence 44, Appli
27	23.4	93.6	43	9	US-10-151-690-19	Sequence 19, Appli
28	23.4	93.6	120	14	US-10-023-208-63	Sequence 63, Appli
29	23.4	93.6	1846	14	US-10-241-596-137	Sequence 137, App
30	23.4	93.6	5558	12	US-10-151-690-20	Sequence 20, Appli
31	23.4	93.6	6464	14	US-10-887-576-581	Sequence 581, App
32	23.4	93.6	11180	10	US-09-855-001A-25	Sequence 25, Appli
33	23.4	93.6	17458	14	US-10-055-001A-25	Sequence 25, Appli
34	23.4	93.6	17476	12	US-10-385-546-7	Sequence 7, Appli
35	23.4	93.6	17476	12	US-10-385-546-7	Sequence 7, Appli
36	23.4	93.6	17476	14	US-10-055-001A-24	Sequence 24, Appli
37	23.4	93.6	17476	14	US-10-055-001A-24	Sequence 24, Appli
38	23.4	93.6	17681	14	US-10-055-001A-26	Sequence 26, Appli
39	23.4	93.6	17681	14	US-10-055-001A-26	Sequence 26, Appli
40	22.6	90.4	25	9	US-09-855-797A-42	Sequence 42, Appli
41	22.6	90.4	25	10	US-09-907-900-42	Sequence 42, Appli
42	22.6	90.4	25	10	US-09-907-719-42	Sequence 42, Appli
43	22.6	90.4	25	12	US-09-985-448-42	Sequence 42, Appli
44	22.6	90.4	25	12	US-10-300-892-42	Sequence 42, Appli
45	22.4	89.6	25	9	US-09-855-797A-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1

US-09-855-797A-10
; Sequence 10, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-10

Query Match 100.0%; Score 25; DB 9; Length 25;

Best Local Similarity 100.0%; Pred.No. 0.089; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTCTGTGACAAACTGT 25

DB 1 GTTCAGCTTCTGTGACAAACTGT 25

RESULT 2

```

VERSION      AX269140.1  GI:16542060
KEYWORDS
SOURCE       synthetic construct
ORGANISM     synthetic construct
             artificial sequences.
REFERENCE    1
AUTHORS      Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
TITLE        Compositions and methods for tissue specific gene regulation
             therapy
JOURNAL      Patent: WO 0174861-A 11 11-OCT-2001;
             MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES     source
             Location/Qualifiers
             1..25
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
             /note="Synthetically generated vector sequence"
BASE COUNT   6 a 6 c 5 g 8 t
ORIGIN
Query Match      88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
    |||||
Db 4 CAGCTTCTCTGTACAAAGTTGG 25
    |||||

RESULT 39
AX491653
LOCUS        AX491653                25 bp DNA linear PAT 16-AUG-2002
DEFINITION   Sequence 14 from Patent EP1227147.
ACCESSION    AX491653
VERSION      AX491653.1  GI:22324161
KEYWORDS
SOURCE       unidentified
ORGANISM     unidentified
             unclassified.
REFERENCE    1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE        Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1227147-A 14 31-JUL-2002;
             INVITROGEN CORPORATION (US)
FEATURES     source
             Location/Qualifiers
             1..25
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
BASE COUNT   6 a 6 c 5 g 8 t
ORIGIN
Query Match      88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
    |||||
Db 4 CAGCTTCTCTGTACAAAGTTGG 25
    |||||

RESULT 40
AX498624
LOCUS        AX498624                25 bp DNA linear PAT 26-SEP-2002
DEFINITION   Sequence 14 from Patent EP1229113.
ACCESSION    AX498624
VERSION      AX498624.1  GI:23343421
KEYWORDS
SOURCE       unidentified
ORGANISM     unidentified
             unclassified.
REFERENCE    1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE        Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1229113-A 14 07-AUG-2002;
             INVITROGEN CORPORATION (US)
FEATURES     source
             Location/Qualifiers
             1..25
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
BASE COUNT   6 a 6 c 5 g 8 t
ORIGIN
Query Match      88.0%; Score 22; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTCTCTGTACAAAGTTGG 25
    |||||
Db 4 CAGCTTCTCTGTACAAAGTTGG 25
    |||||

Search completed: November 6, 2003, 23:06:43
Job time : 602 secs

```

```

/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT      3343 a   3271 c   3178 g   3482 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 13274;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTG 24
|||||
Db 2370 GTTCAGCTTCTTGTACAAAGTTG 2347
|||||

RESULT 35
AF541939      13990 bp      DNA      linear      SYN 01-DEC-2002
LOCUS
DEFINITION His-3 integration vector pJHAM007, complete sequence.
ACCESSION AF541939
VERSION AF541939.1 GI:25988997
KEYWORDS his-3 integration vector pJHAM007
SOURCE his-3 integration vector pJHAM007
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Description of a GATEWAY Destination Vector For High-Throughput
Construction of Neurospora crassa Histidine-3 (his-3)-Gene
Replacement Plasmids
FEATURES
Unpublished
2 (bases 1 to 13990)
Haag,J.R., Lee,D.W. and Aramayo,R.
Direct Submission
Submitted (27-AUG-2002) Biology, Texas A&M University, BSEW #415,
College Station, TX 77843-3258, USA
LOCUS
LOCATION/Qualifiers
1..13990
/organism="his-3 integration vector pJHAM007"
/mol_type="genomic DNA"
/specific host="Neurospora crassa"
/db_xref="taxon:211505"
1..3173
/notes="pGEM13zf(+)"
misc_feature 3174..8368
/notes="his-3 left flank; his-3 target integration site"
misc_feature 8430..8554
/notes="attR1; Gateway; Bacteriophage Lambda recombination
site"
CDS
8804..9463
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="AA076304.1"
/db_xref="GI:25988998"
translation="MEKKITGVTVTDISOWHKEHEPEAFQSAQCTYQCTVQVLDITAF
LTKVKKHKHFYAPFHILARLNARPEFRAMKOGELVINDSVHPCHYTVFHEQETTF
SLMSYHDDFQFLHIYSDVACGENLAYFPKFIENMFVSNPVSFTSFDLNV
ANMNDFFAVFTNGKYTGQDKVLMPLAIQVHHAUCDGFHVGRLMELQQYCDWEQGG
A"
89805..10110
/notes="ccdB"
misc_feature 10419..13990
/notes="his-3 right flank; his-3 target integration site"
BASE COUNT      3385 a   3549 c   3559 g   3497 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 13274;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTGTACAAAGTTG 24
|||||
Db 2370 GTTCAGCTTCTTGTACAAAGTTG 2347
|||||

RESULT 35
AF541939      13990 bp      DNA      linear      SYN 01-DEC-2002
LOCUS
DEFINITION His-3 integration vector pJHAM007, complete sequence.
ACCESSION AF541939
VERSION AF541939.1 GI:25988997
KEYWORDS his-3 integration vector pJHAM007
SOURCE his-3 integration vector pJHAM007
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Description of a GATEWAY Destination Vector For High-Throughput
Construction of Neurospora crassa Histidine-3 (his-3)-Gene
Replacement Plasmids
FEATURES
Unpublished
2 (bases 1 to 13990)
Haag,J.R., Lee,D.W. and Aramayo,R.
Direct Submission
Submitted (27-AUG-2002) Biology, Texas A&M University, BSEW #415,
College Station, TX 77843-3258, USA
LOCUS
LOCATION/Qualifiers
1..13990
/organism="his-3 integration vector pJHAM007"
/mol_type="genomic DNA"
/specific host="Neurospora crassa"
/db_xref="taxon:211505"
1..3173
/notes="pGEM13zf(+)"
misc_feature 3174..8368
/notes="his-3 left flank; his-3 target integration site"
misc_feature 8430..8554
/notes="attR1; Gateway; Bacteriophage Lambda recombination
site"
CDS
8804..9463
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="AA076304.1"
/db_xref="GI:25988998"
translation="MEKKITGVTVTDISOWHKEHEPEAFQSAQCTYQCTVQVLDITAF
LTKVKKHKHFYAPFHILARLNARPEFRAMKOGELVINDSVHPCHYTVFHEQETTF
SLMSYHDDFQFLHIYSDVACGENLAYFPKFIENMFVSNPVSFTSFDLNV
ANMNDFFAVFTNGKYTGQDKVLMPLAIQVHHAUCDGFHVGRLMELQQYCDWEQGG
A"
89805..10110
/notes="ccdB"
misc_feature 10419..13990
/notes="his-3 right flank; his-3 target integration site"
BASE COUNT      3385 a   3549 c   3559 g   3497 t
ORIGIN

```

```
/organism="piggyBac transformation vector pB-UGIR w+"
/mol_type="genomic DNA"
/db_xref="taxon:221642"
complement(11..>620)
/transposon="piggyBac transposable element"
632..998
/feature="5x UAS hsp70 TATA signal"
1003..2713
/feature="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
2726..3040
/feature="RpSS"
/number=3
complement(3076..4788)
/transposon="Gateway recombination cassette B; attR1 CmR ccdB
attR2"
4789..5246
/feature="SV40"
5247..9369
/feature="w"
/feature="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTACAAAGTTG 24
|||||
Db 2686 GTTCAGCTTCTGTACAAAGTTG 2709
|||||
RESULT 32
AY196825/c
LOCUS AY196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
source
1..12677
Location/Qualifiers
/organism="piggyBac transformation vector pB-UGIR w+"
/mol_type="genomic DNA"
/db_xref="taxon:221642"
complement(11..>620)
/transposon="piggyBac transposable element"
632..998
/feature="5x UAS hsp70 TATA signal"
1003..2713
/feature="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
2726..3040
/feature="RpSS"
/number=3
complement(3076..4788)
/transposon="Gateway recombination cassette B; attR1 CmR ccdB
attR2"
4789..5246
/feature="SV40"
5247..9369
/feature="w"
/feature="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTACAAAGTTG 24
|||||
Db 2686 GTTCAGCTTCTGTACAAAGTTG 2709
|||||
RESULT 32
AY196825/c
LOCUS AY196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
source
1..12677
Location/Qualifiers
/organism="piggyBac transformation vector pB-UGIR w+"
/mol_type="genomic DNA"
/db_xref="taxon:221642"
complement(11..>620)
/transposon="piggyBac transposable element"
632..998
/feature="5x UAS hsp70 TATA signal"
1003..2713
/feature="Gateway recombination cassette A; attR1 CmR ccdB
attR2"
2726..3040
/feature="RpSS"
/number=3
complement(3076..4788)
/transposon="Gateway recombination cassette B; attR1 CmR ccdB
attR2"
4789..5246
/feature="SV40"
5247..9369
/feature="w"
/feature="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
ORIGIN
```

```
polya_signal 4789..5246
/feature="SV40"
5247..9369
/feature="w"
/feature="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"
BASE COUNT 3423 a 2924 c 2833 g 3497 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTACAAAGTTG 24
|||||
Db 3104 GTTCAGCTTCTGTACAAAGTTG 3081
|||||
RESULT 33
AX590202/c
LOCUS AX590202 12789 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION AX590202
VERSION AX590202.1 GI:27901286
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Goossens,A. and Inz,D.
TITLE The use of genes encoding membrane transporter pumps to stimulate
the production of secondary metabolites in biological cells
JOURNAL Patent: WO 02083888-A 9 24-OCT-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
source
1..12789
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/feature="vector pK7WG2D"
BASE COUNT 3050 a 3326 c 3397 g 3015 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 12789;
Best Local Similarity 95.8%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTGTACAAAGTTG 24
|||||
Db 2045 GTTCAGCTTCTGTACAAAGTTG 2022
|||||
RESULT 34
AX356862/c
LOCUS AX356862 13274 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 20 from Patent WO0206490.
ACCESSION AX356862
VERSION AX356862.1 GI:18674110
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Dudler,R., Schaffrath,U. and Lawton,K.A.
TITLE Lipoxigenase genes, promoters, transit peptides and proteins
thereof
JOURNAL Patent: WO 0206490-A 20 24-JAN-2002;
Syngenta Participations AG (CH); Universitaet Zuerich (CH)
FEATURES
source
1..13274
Location/Qualifiers
/organism="synthetic construct"
```

```

LKTVMKXKHKFYPAFIHLARLMAHAEFRFAMKDGELVIWDSVHPCHYTVFHEQTETFF
SSLSWSEHDDFRFLHYSDVACYGENLAYFPKGFIEFNMFVFSANPWFSTFSDLNV
ANMNDFFAPFTWTKYTGQDKVLMPLAIQVHHAUCDGFHVGRLNELQYCDWEQGG
A"
1263. 1568
/genes="ccdB"
1263. 1568
/genes="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62301.1"
/db_xref="GI:21552738"
/translational="MQPKVITYKRESRYRLFVDVQSDIIDTPGRRMVIPLASRLISD
KVSRELYPVVHIGDESRWMTTDMASVPVSVIGEEVADLSHRENDIKNALNMFWGI"
1610. 1736
/notes="attR2 of Gateway conversion cassette frame A"
1762. 2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
/complement(2073. 3783)
/notes="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, Cmr gene and
ccdB gene"
misc_feature
complement(2073. 2199)
/notes="attR2 of Gateway conversion cassette frame A"
gene
complement(2241. 2546)
/genes="ccdB"
CDS
complement(2241. 2546)
/genes="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62303.1"
/db_xref="GI:21552740"
/translational="MQPKVITYKRESRYRLFVDVQSDIIDTPGRRMVIPLASRLISD
KVSRELYPVVHIGDESRWMTTDMASVPVSVIGEEVADLSHRENDIKNALNMFWGI"
complement(2888. 3547)
/genes="Cmr"
CDS
complement(2888. 3547)
/genes="Cmr"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62302.1"
/db_xref="GI:21552739"
/translational="MEKKITGYTVDISQWHRKEHFEAFQSVACQYNTVQLDITAF
LKTVMKXKHKFYPAFIHLARLMAHAEFRFAMKDGELVIWDSVHPCHYTVFHEQTETFF
SSLSWSEHDDFRFLHYSDVACYGENLAYFPKGFIEFNMFVFSANPWFSTFSDLNV
ANMNDFFAPFTWTKYTGQDKVLMPLAIQVHHAUCDGFHVGRLNELQYCDWEQGG
A"
complement(3657. 3783)
misc_feature
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 9019;
Best Local Similarity 95.8%; Pred. No. 4.6;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTGG 24
Db 2100 GTTCAGCTTCTTGTCACAAAGTGG 2077
RESULT 30
LOCUS AY196824
DEFINITION PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION AY196824

```

```

VERSION AY196824.1 GI:28565716
KEYWORDS piggyBac transformation vector pB-UGateway w+
SOURCE piggyBac transformation vector pB-UGateway w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
source
location/Qualifiers
1..11005
/organism="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..>620)
repeat_region
/transposon="piggyBac transposable element"
TATA_signal
643..999
misc_feature
/notes="5x UAS hsp70 TATA signal"
1003..2713
/notes="Gateway recombination cassette A; attR1 Cmr ccdB
attR2"
intron
2726..3040
/number=3
polyA_signal
3072..3573
gene
3574..7697
/notes="SV40"
/genes="w"
repeat_region
/notes="mini-white; derived from Drosophila"
complement(<7698..8147)
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 11005;
Best Local Similarity 95.8%; Pred. No. 4.5;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGTCACAAAGTGG 24
Db 2686 GTTCAGCTTCTTGTCACAAAGTGG 2709
RESULT 31
LOCUS AY196825
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
KEYWORDS piggyBac transformation vector pB-UGIR w+
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
source
location/Qualifiers
1..12677

```


Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTACAAAGTTG 24
 |||||
 Db 1822 GTTCAGCTTTCTTGTACAAAGTTG 1845

RESULT 26
 VFO551314 4462 bp DNA circular SYN 27-MAR-2003
 LOCUS Transfection vector pBrdet.
 AJ551314
 VERSION AJ551314.1 GI:29335742
 KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol acetyl transferase; control of cell death B protein.
 SOURCE Transfection vector pBrdet
 ORGANISM artificial sequences; vectors.
 REFERENCE 1
 AUTHORS Jakob, M.J., Heim, M.A. and Weishaar, B.
 TITLE Use of a gateway compatible vector for transient plant transfection
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4462)
 AUTHORS Jakob, M.J.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAR-2003) Jakob M.J., Salamini, MPI for Plant Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
 FEATURES
 source
 1..4462
 /organism="Transfection vector pBrdet"
 /mol_type="genomic DNA"
 /db_xref="taxon:225975"
 31..443
 /note="35S"
 421..424
 /note="35S"
 456..580
 /note="attR1"
 689..1348
 /genes="cat"
 689..1348
 /genes="cat"
 /codon_start=1
 /product="chloramphenicol acetyl transferase"
 /protein_id="CAD83080.1"
 /db_xref="GI:29335743"
 /translations="MEKKITGYTTVDISOWHRRKEHFEAFOSVAQCTYNQTVOLDITAF LKTVKNKHKFPFATHILARLNAHPEFRMAKDGELVWDSVHPCYTVFHEQTEF SSLWSVHDDFROFLHYSDVACVGENLAYFPKGIENFFVSANPWFVTSFDLNV ANMDNFPAPFTMGKYYTQGDVKVIMPLAIQVHHAUCDGFHVGRLNELQQYCDWEQGG A"
 1690..1995
 /genes="ccdB"
 1690..1995
 /genes="ccdB"
 /codon_start=1
 /product="control of cell death B protein"
 /protein_id="CAD83081.1"
 /db_xref="GI:29335744"
 /translations="MGPKVTVKRSRYRLFVDVQSDIIDTPGRRWVPIASARLLSD KVSRELYPVVHIGDESRRMTTDMASVPVSVIGEEVADLSHRENDKNAINLPWGI"
 2036..2160
 /note="attR2"
 2168..2463
 /genes="noet"
 2168..2463
 /genes="noet"
 2606..3466
 /genes="amp"
 2606..3466
 /genes="amp"
 /codon_start=1
 /product="beta lactamase"

BASE COUNT 1223 a 995 c 1065 g 1179 t
 ORIGIN

Query Match 89.6%; Score 22.4; DB 12; Length 4462;
 Best Local Similarity 95.8%; Pred. No. 5;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTACAAAGTTG 24
 |||||
 Db 2136 GTTCAGCTTTCTTGTACAAAGTTG 2159

RESULT 27
 AX306327 5148 bp DNA linear PAT 11-DEC-2001
 LOCUS Sequence 10 from Patent WO0188121.
 AX306327
 VERSION AX306327.1 GI:17645566
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Plaetinck, G., Renard, J.P. and Bogaert, T.
 TITLE Vector constructs
 JOURNAL Patent: WO 0188121-A 10 22-NOV-2001;
 Devgen NV (BE)
 FEATURES
 Location/Qualifiers
 source
 1..5148
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Plasmid pGN39"
 BASE COUNT 1359 a 1199 c 1279 g 1311 t
 ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 5148;
 Best Local Similarity 95.8%; Pred. No. 4.9;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTTGTACAAAGTTG 24
 |||||
 Db 1827 GTTCAGCTTTCTTGTACAAAGTTG 1850

RESULT 28
 AF408413 9019 bp DNA circular SYN 25-JUN-2002
 LOCUS Binary vector pJawohl8-RNAi, complete sequence.
 AF408413
 VERSION AF408413.1 GI:21552736
 KEYWORDS Binary vector pJawohl8-RNAi
 SOURCE Binary vector pJawohl8-RNAi
 ORGANISM artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somsich, I.E.
 TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somsich, I.E.
 TITLE Direct Submission
 JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829, Germany


```

RESULT 22
AX498620
LOCUS AX498620
DEFINITION Sequence 10 from Patent EP1229113.
ACCESSION AX498620
VERSION AX498620.1 GI:23343417
KEYWORDS
ORGANISM
SOURCE
REFERENCE
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 10 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24
|||||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 23
BD131336
LOCUS BD131336
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131336
VERSION BD131336.1 GI:23226281
KEYWORDS JP 2002500861-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1..25
/organism='Unknown'.
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24
|||||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 24
AX498620
LOCUS AX498620
DEFINITION Sequence 10 from Patent EP1229113.
ACCESSION AX498620
VERSION AX498620.1 GI:23343417
KEYWORDS
ORGANISM
SOURCE
REFERENCE
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 10 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24
|||||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 25
AX703501
LOCUS AX703501
DEFINITION Sequence 63 from Patent WO02066653.
ACCESSION AX703501
VERSION AX703501.1 GI:29538461
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
AUTHORS Li,M. and Liu,Y.C.
TITLE Procarvotic libraries and uses
JOURNAL Patent: WO 02066653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
source
1..1846
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 527 a 381 c 434 g 504 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 1846;
Best Local Similarity 95.8%; Pred. No. 5.5;

```

```

|||||
1 GTTCAGCTTCTTGACAAAGTTG 24

BD131337
LOCUS BD131337
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131337
VERSION BD131337.1 GI:23226282
KEYWORDS JP 2002500861-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 11 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/11
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1..25
/organism='Unknown'.
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 9.1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAAGTTG 24
|||||
Db 1 GTTCAGCTTCTTGACAAAGTTG 24

RESULT 25
AX703501
LOCUS AX703501
DEFINITION Sequence 63 from Patent WO02066653.
ACCESSION AX703501
VERSION AX703501.1 GI:29538461
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
AUTHORS Li,M. and Liu,Y.C.
TITLE Procarvotic libraries and uses
JOURNAL Patent: WO 02066653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
source
1..1846
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 527 a 381 c 434 g 504 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 6; Length 1846;
Best Local Similarity 95.8%; Pred. No. 5.5;

```



```

Db      14520 GTTCAGCTTCTTGACAAAGTTGG 14544
|||||
RESULT 12
CUE311874/c
LOCUS   CUE311874          18691 bp      DNA      circular SYN 09-JUL-2002
DEFINITION Cloning vector pHELLSGATE.
ACCESSION AJ311874
VERSION   AJ311874.1 GI:15982218
KEYWORDS  kanomycin resistance protein; neomycin phosphotransferase II; nptII
          gene; promoter; spec gene; spectinomycin resistance protein;
          transposon Tn7.
SOURCE   Cloning vector pHELLSGATE
ORGANISM Cloning vector pHELLSGATE
          artificial sequences; vectors.
REFERENCE
AUTHORS   Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
          Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
          Gleave,A.P., Green,A.G. and Waterhouse,P.M.
          Construct design for efficient, effective and high-throughput gene
          silencing in plants
JOURNAL   Plant J. 27 (6), 581-590 (2001)
MEDLINE   21461301
PUBMED    11576441
REFERENCE
AUTHORS   Waterhouse,P.M.
          Direct Submission
TITLE     Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
          C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
JOURNAL
FEATURES
source    1. .18691
          /organism="Cloning vector pHELLSGATE"
          /mol_type="genomic DNA"
          /db_xref="taxon:167049"
          /lab_host="Escherichia coli"
          /focus
          /notes="pHELLSGATE is a derivative of cloning vector
          PART2"
source    1. .264
          /organism="Escherichia coli K12"
          /mol_type="genomic DNA"
          /strain="K12"
          /db_xref="taxon:83333"
          /db_xref="taxon:83333"
          265. .448
          /organism="Agrobacterium tumefaciens"
          /mol_type="genomic DNA"
          /db_xref="taxon:358"
          /db_xref="taxon:358"
          449. .1442
          /organism="Escherichia coli"
          /mol_type="genomic DNA"
          /db_xref="taxon:562"
          /db_xref="taxon:562"
          1443. .7792
          /organism="Agrobacterium tumefaciens"
          /mol_type="genomic DNA"
          /db_xref="taxon:358"
          /db_xref="taxon:358"
          7793. .9388
          /organism="Escherichia coli"
          /mol_type="genomic DNA"
          /db_xref="taxon:562"
          /db_xref="taxon:562"
          9389. .11673
          /organism="Agrobacterium tumefaciens"
          /mol_type="genomic DNA"
          /db_xref="taxon:358"
          /db_xref="taxon:358"
          11674. .13019
          /organism="Cauliflower mosaic virus"
          /mol_type="genomic DNA"
          /db_xref="taxon:10641"
          /db_xref="taxon:10641"
          14660. .16258
          /organism="Flaveria trinervia"
          /mol_type="genomic DNA"
          /db_xref="taxon:4227"
          /db_xref="taxon:4227"
          17922. .18691

```

```

/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
264. .447
/function="NOS promoter"
448. .1269
/gene="nptII"
448. .1269
/gene="nptII"
/codon_start=1
/codon="neomycin phosphotransferase II (nptII)"
/transl_table=11
/product="kanomycin resistance protein"
/protein_id="CAC86252.1"
/db_xref="GI:15982219"
/db_xref="REMTREMBL:CAC86252"
/translation="MAITLSATSLPISARIRAGSPAAWVERLFGVDMQOITGCSDA
VERLSAQGRPVLFVKIDLSGALNELQDEARLRLNLTATGVPCAALVDVTERGRDMLL
LGEVPGQLLSHLLAPAEKVSIMADAMRLRLDLPDFFDQAKHRIENRGRFMEAG
LVDQDLDEHGGGLAPAEFLFARLKARMPDGEDLVVTHGDACLPLNINVENRFGSGFIDC
GRLGVADRYQDIALATRDIAELGGEWADRFIVLYGIAAPDSQRIAFVRLIDEFF"
1443. .2148
/terminator
/notes="NOS terminator"
2149. .2706
/repeat_region
/notes="left border"
7793. .9388
/transposon="Tn7"
8600. .9388
/gene="spec"
8600. .9388
/gene="spec"
/codon_start=1
/transl_table=11
/product="spectinomycin resistance protein"
/protein_id="CAC86253.1"
/db_xref="GI:15982220"
/db_xref="REMTREMBL:CAC86253"
/translation="MREAVIAEVSTQSEVGVIERHLEPTLLAVHLYGSADVGGKLP
HSDIDLVTVRLDETTRALLNDLLETSPGSEILRAVEVTIVHDDIIPWRYP
AKRELQFGWQRNDILAGIFEPATIDIDLAILTKARHSAVALGPAABELFDPVPEQ
DLFEALNETLTLWNSPPDWAGDNRNVLTLSRIWYSAVTGKIAPKDVAADWAMERLPA
QYQPVLEARQAVLQGEDRLASRAQDLBEFVHVYKGEITKVYVK"
10706. .11324
/repeat_region
/notes="right border"
11674. .13019
/function="35S promoter"
14660. .16258
/gene="pdk"
14660. .16258
/gene="pdk"
/notes="pyruvate orthophosphate dikinase (pdk)"
/number=2
/terminator
17922. .18687
/notes="octopine esynthase (ocs) terminator"
BASE COUNT 4837 a 4621 c 4607 g 4626 t
ORIGIN
Query Match 100.0%; Score 25; DB 12; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTCTTGACAAAGTTGG 25
|||||
Db 16418 GTTCAGCTTCTTGACAAAGTTGG 16394
|||||
RESULT 13
BD131369
LOCUS BD131369 25 bp DNA linear PAT 19-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131369
VERSION BD131369.1 GI:23226314

```

```

/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
5 a 4 c 6 g 10 t

BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAAAGTTGG 25
DB 1 GTTCAGCTTCTGTGACAAAGTTGG 25

RESULT 11
CV311874 18691 bp DNA circular SYN 09-JUL-2002
LOCUS Cloning vector pHELLSGATE.
DEFINITION AJ311874
ACCESSION AJ311874.1 GI:15982218
VERSION kanomycin resistance protein; neomycin phosphotransferase II; nptII
KEYWORDS gene; promoter; spec gene; spectinomycin resistance protein;
transposon Tn7.
SOURCE Cloning vector pHELLSGATE
ORGANISM Cloning vector pHELLSGATE
artificial sequences; vectors.
REFERENCE 1
AUTHORS Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
Gooding,ps., Singh,S.R., Abbott,D., Scoufjesdij,k,A., Robinson,S.P.,
Gleave,A.P., Green,A.G. and Waterhouse,P.M.
TITLE Construct design for efficient, effective and high-throughput gene
silencing in plants
JOURNAL Plant J. 27 (6), 581-590 (2001)
MEDLINE 21461301
PUBMED 11576441
REFERENCE 2 (bases 1 to 18691)
AUTHORS Waterhouse,P.M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
FEATURES
source
1..18691
Location/Qualifiers
/organism="Cloning vector pHELLSGATE"
/mol_type="genomic DNA"
/db_xref="taxon:167049"
/lab_host="Escherichia coli"
/focus="pHELLSGATE is a derivative of cloning vector
pART27"
source
1..264
/organism="Escherichia coli K12"
/mol_type="genomic DNA"
/strain="K12"
/db_xref="taxon:83333"
265..448
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
449..1442
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
1443..7792
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
7793..9388
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
9389..11673
/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"
/db_xref="taxon:358"
11674..13019
/organism="Cauliflower mosaic virus"
/mol_type="genomic DNA"
/db_xref="taxon:10641"
14660..16258
/organism="Flaveria trinervia"
/mol_type="genomic DNA"
/db_xref="taxon:4227"
17922..18691
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"
264..447
/function="NOS promoter"
448..1269
/gene="nptII"
448..1269
/gene="nptII"
/note="neomycin phosphotransferase II (nptII)"
/codon_start=1
/transl_table=11
/product="kanomycin resistance protein"
/protein_id="CAC86252.1"
/db_xref="GI:15982219"
/db_xref="REMTREMBL:CAC86252"
/translation="MAITLSATSLPISARIRAGSPAAWVERLFGVDNAQQTIGGSDAA
VFRISAQRPVLFVKTLDSGALNEQDEARLSMLATGVCAAVLDVVTAGRDWLL
LGVDFQDLSHSLPAEKVSIMADAMRLHLDLPATCFDQAKHRLERAGRKEAG
LVDDDLDEHQGLAPAEFLPARLKMDFGDLVVTGDACLPIMVNGRFSGFIDC
GRLGVDYQDIATATRDIAELGGEWADFVLVLYGIAAPDSQRTAFYRLILDEFF"
1443..2148
/note="NOS terminator"
2149..2706
/note="left border"
7793..9388
/transposon="Tn7"
8600..9388
/gene="spec"
9600..9388
/gene="spec"
/codon_start=1
/transl_table=11
/product="spectinomycin resistance protein"
/protein_id="CAC86253.1"
/db_xref="GI:15982220"
/db_xref="REMTREMBL:CAC86253"
/translation="MREAVIAEVSTQLSEVGVTERHLEPTLLAHLVYGSVDGGLKP
HSDIDLIVTVRLDDETRRALINDLSTASPGSEITLRAVEVTVVHDDIIPWRYP
AKRELQFGWQRNDILAGIFFPATIDIDLAILTKAREHVALGPAAEELFDVPEQ
DLFEALNETLTLMNSPPDWAGDNRNVLTLSRIWYSVATGKIAPKDAADWAMERLPA
QYQVILEARQYLQEDRLASRAQDLEEFVHYVKGKITKVVGK"
10706..11324
/note="right border"
11674..13019
/function="35S promoter"
14660..16258
/gene="pdk"
14660..16258
/gene="pdk"
/note="pyruvate orthophosphate dikinase (pdk)"
/number=2
17922..18687
/note="octopine esynthase (ocs) terminator"
BASE COUNT 4837 a 4621 c 4607 g 4626 t
ORIGIN
Query Match 100.0%; Score 25; DB 12; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTGTGACAAAGTTGG 25

```

AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 11 31-JUL-2002;
INVITROGEN CORPORATION (US)

FEATURES
source Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 10 t

BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 7
AX491655
LOCUS AX491655 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 16 from Patent EP1227147.
ACCESSION AX491655
VERSION AX491655.1 GI:22324163
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)

FEATURES
source Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 10 t

BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 8
AX498621
LOCUS AX498621 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 11 from Patent EP1229113.
ACCESSION AX498621
VERSION AX498621.1 GI:23343418
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 11 07-AUG-2002;
INVITROGEN CORPORATION (US)

FEATURES
source Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.49; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 9
AX498626
LOCUS AX498626 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 16 from Patent EP1229113.
ACCESSION AX498626
VERSION AX498626.1 GI:23343423
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 16 07-AUG-2002;
INVITROGEN CORPORATION (US)

FEATURES
source Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 10 t

BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.49; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

RESULT 10
BD131342
LOCUS BD131342 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131342
VERSION BD131342.1 GI:23226287
KEYWORDS JP 2002500861-A/16.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination sites
JOURNAL Patent: JP 2002500861-A 16 15-JAN-2002;
LIFE TECHNOLOGIES INC

COMMENT
OS UNKNOWN
PN JP 2002500861-A/16
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI

CC 12N15/09, C12Q1/68, C12N15/00
C12N15/09, C12Q1/68, C12N15/00
CC Description of unknown Organism: recombination products PH
Key Location/Qualifiers
FT source 1..25
FT /organism='Unknown'.
FT Location/Qualifiers
1..25

FEATURES
source

```

source
1. .25
/organism="unknown"
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 2
AR124536
LOCUS AR124536 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 16 from patent US 6171861.
ACCESSION AR124536
VERSION AR124536.1 GI:14109897
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 16 09-JAN-2001;
FEATURES
Location/Qualifiers
1. .25
/organism="unknown"
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 3
AR163182
LOCUS AR163182 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 11 from patent US 6270969.
ACCESSION AR163182
VERSION AR163182.1 GI:162233692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 11 07-AUG-2001;
FEATURES
Location/Qualifiers
1. .25
/organism="unknown"
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 4
AR163187
LOCUS AR163187 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 16 from patent US 6270969.
ACCESSION AR163187
VERSION AR163187.1 GI:162233699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 16 07-AUG-2001;
FEATURES
Location/Qualifiers
1. .25
/organism="unknown"
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 5
AX269137
LOCUS AX269137 25 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 8 from Patent WO0174861.
ACCESSION AX269137
VERSION AX269137.1 GI:16542057
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
Compositions and methods for tissue specific gene regulation
therapy
Patent: WO 0174861-A 8 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetically generated vector sequence"
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 25; DB 6; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGTCACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTCTTGTCACAAAGTTGG 25

RESULT 6
AX491650
LOCUS AX491650 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 11 from Patent EP1227147.
ACCESSION AX491650
VERSION AX491650.1 GI:22324158
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-11

Perfect score: 25
Sequence: 1 gttcagctttctgtacaaagtgg 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_man:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	25	100.0	25	6	AR124531 Sequence
2	25	100.0	25	6	AR124536 Sequence
3	25	100.0	25	6	AR163182 Sequence
4	25	100.0	25	6	AR163187 Sequence
5	25	100.0	25	6	AX269137 Sequence
6	25	100.0	25	6	AX491650 Sequence
7	25	100.0	25	6	AX491655 Sequence
8	25	100.0	25	6	AX498621 Sequence
9	25	100.0	25	6	AX498626 Sequence
10	25	100.0	25	6	BD131342 Sequence
11	25	100.0	18691	12	CVE311874
12	25	100.0	18691	12	CVE311874
13	23.8	95.2	25	6	BD131369 Sequence
14	23.4	93.6	25	6	AR124535 Sequence
15	23.4	93.6	25	6	AR163186 Sequence
16	23.4	93.6	25	6	AX491654 Sequence
17	23.4	93.6	25	6	AX498625 Sequence
18	23.4	93.6	25	6	BD131341 Sequence
19	22.4	89.6	25	6	AR124530 Sequence
20	22.4	89.6	25	6	AR163181 Sequence
21	22.4	89.6	25	6	AX491649 Sequence
22	22.4	89.6	25	6	AX498620 Sequence
23	22.4	89.6	25	6	BD131336 Sequence
24	22.4	89.6	25	6	BD131337 Sequence
25	22.4	89.6	1846	6	AX703501 Sequence
26	22.4	89.6	4462	12	VFO551314
27	22.4	89.6	5148	6	AX306327 Sequence
28	22.4	89.6	9019	12	AF408413
29	22.4	89.6	9019	12	AF408413
30	22.4	89.6	11005	12	AY196824 PiggyBac
31	22.4	89.6	12677	12	AY196825 PiggyBac
32	22.4	89.6	12677	12	AY196825 PiggyBac
33	22.4	89.6	12789	6	AX590202 Sequence
34	22.4	89.6	13274	6	AX356862 Sequence
35	22.4	89.6	13990	12	AF541939 His-3 int
36	22	88.0	25	6	AR124534 Sequence
37	22	88.0	25	6	AR163185 Sequence
38	22	88.0	25	6	AX269140 Sequence
39	22	88.0	25	6	AX491653 Sequence
40	22	88.0	25	6	AX498624 Sequence
41	22	88.0	25	6	BD131340 Sequence
42	22	88.0	25	6	BD131368 Sequence
43	20.8	83.2	25	6	AR124529 Sequence
44	20.8	83.2	25	6	AR163180 Sequence
45	20.8	83.2	25	6	AX269136 Sequence

ALIGNMENTS

RESULT 1
AR124531
LOCUS AR124531
DEFINITION Sequence 11 from patent US 6171861.
ACCESSION AR124531
VERSION AR124531.1 GI:114109892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
FEATURES Location/Qualifiers

AR124531 25 bp DNA linear PAT 16-MAY-2001

/tissue type="whole animal"
/dev stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 32 a 18 c 22 g 39 t
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 111;
Best Local Similarity 95.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
|||||
Db 71 CAGCTTCTGTGACAAAGTTGG 92
|||||

Search completed: November 7, 2003, 00:21:00
Job time : 1096.75 secs

Query Match 81.6%; Score 20.4; DB 14; Length 111;
Best Local Similarity 95.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
|||||
Db 71 CAGCTTCTGTGACAAAGTTGG 92
|||||

RESULT 40
CB395510/c
LOCUS 111 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR1508A1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395510
VERSION CB395510.1 GI:30737221
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 111)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.,
Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression

Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact David Hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.

FEATURES
source
1..111
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 28 a 26 c 19 g 38 t
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 111;

Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA-No.

FEATURES
source
Location/Qualifiers
1. .106
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A) +
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
29 a 21 c 12 g 44 t

BASE COUNT
ORIGIN
Query Match 81.6%; Score 20.4; DB 14; Length 106;
Best Local Similarity 95.5%; Pred. No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
|||||
Db 40 CTGCTTTTGTACAAAGTTGG 19
|||||

RESULT 38
CB388456/c
LOCUS 107 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTRF099E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB388456
VERSION CB388456.1 GI:30730166
KEYWORDS EST.
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 107)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA-No.

FEATURES
source
Location/Qualifiers
1. .107
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A) +
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
34 a 18 c 16 g 39 t

BASE COUNT
ORIGIN
Query Match 81.6%; Score 20.4; DB 14; Length 107;
Best Local Similarity 95.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
|||||
Db 29 CAGCTTTTGTACAAAGTTGG 8
|||||

RESULT 39
CB394444
LOCUS 111 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR137H4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB394444
VERSION CB394444.1 GI:30736155
KEYWORDS EST.
SOURCE
ORGANISM
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 111)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA-No.

FEATURES
source
Location/Qualifiers
1. .111
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"

Matches	21; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
QY	4	CAGCTTTTGTGACAAAGTTGG	25		
Db	46	CTGCTTTTGTGACAAAGTTGG	25		
RESULT 35					
CB401874/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
BASE COUNT					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY	4	CAGCTTTTGTGACAAAGTTGG	25		
Db	36	CAGCTTTTCTTGTACAAAGTTGG	15		
RESULT 36					
CB396275/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
BASE COUNT					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY	4	CAGCTTTTGTGACAAAGTTGG	25		
Db	36	CAGCTTTTCTTGTACAAAGTTGG	15		
RESULT 36					
CB396275/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
BASE COUNT					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY	4	CAGCTTTTGTGACAAAGTTGG	25		
Db	36	CAGCTTTTCTTGTACAAAGTTGG	15		
RESULT 36					
CB396275/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
BASE COUNT					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY	4	CAGCTTTTGTGACAAAGTTGG	25		
Db	36	CAGCTTTTCTTGTACAAAGTTGG	15		
RESULT 36					
CB396275/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					

VERSION CB396275.1 GI:30737986
KEYWORDS EST.
ORGANISM Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
REFERENCE 1 (bases 1 to 104)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,
C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevret,E., Papasotiropoulos,V., Toliaas,P.P.,
Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
SOURCE Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 958, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
FEATURES Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project ; Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
LOCATION/Qualifiers POLYA=No.
1..104
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauvers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 30 a 20 c 15 g 39 t
ORIGIN
Query Match 81.6%; Score 20.4; DB 14; Length 104;
Best Local Similarity 95.8%; Pred.No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CAGCTTTTGTGTACAAAGTTGG 25
Db 39 CTGCTTTTGTGTACAAAGTTGG 18
RESULT 37
LOCUS CB396817/c
DEFINITION QSTR179E7.1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
ACCESSION CB396817
VERSION CB396817.1 GI:30738528
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
REFERENCE 1 (bases 1 to 106)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,
C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevret,E., Papasotiropoulos,V., Toliaas,P.P.,
Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
SOURCE Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 958, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
FEATURES Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project ; Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
LOCATION/Qualifiers POLYA=No.
1..104
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauvers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 30 a 20 c 15 g 39 t
ORIGIN
Query Match 81.6%; Score 20.4; DB 14; Length 104;
Best Local Similarity 95.8%; Pred.No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CAGCTTTTGTGTACAAAGTTGG 25
Db 39 CTGCTTTTGTGTACAAAGTTGG 18
RESULT 37
LOCUS CB396817/c
DEFINITION QSTR179E7.1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
ACCESSION CB396817
VERSION CB396817.1 GI:30738528
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
REFERENCE 1 (bases 1 to 106)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,
C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevret,E., Papasotiropoulos,V., Toliaas,P.P.,
Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
SOURCE Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 958, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
FEATURES Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project ; Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
LOCATION/Qualifiers POLYA=No.
1..104
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauvers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 30 a 20 c 15 g 39 t
ORIGIN
Query Match 81.6%; Score 20.4; DB 14; Length 104;
Best Local Similarity 95.8%; Pred.No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CAGCTTTTGTGTACAAAGTTGG 25
Db 39 CTGCTTTTGTGTACAAAGTTGG 18
RESULT 37
LOCUS CB396817/c
DEFINITION QSTR179E7.1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
ACCESSION CB396817
VERSION CB396817.1 GI:30738528
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
REFERENCE 1 (bases 1 to 106)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,
C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevret,E., Papasotiropoulos,V., Toliaas,P.P.,
Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
SOURCE Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 958, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
FEATURES Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project ; Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
LOCATION/Qualifiers POLYA=No.
1..104
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauvers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 30 a 20 c 15 g 39 t
ORIGIN
Query Match 81.6%; Score 20.4; DB 14; Length 104;
Best Local Similarity 95.8%; Pred.No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CAGCTTTTGTGTACAAAGTTGG 25
Db 39 CTGCTTTTGTGTACAAAGTTGG 18
RESULT 37
LOCUS CB396817/c
DEFINITION QSTR179E7.1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 15-MAY-2003
ACCESSION CB396817
VERSION CB396817.1 GI:30738528
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; R

designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu

FEATURES

Location/Qualifiers
1. .102
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 31 a 14 c 22 g 35 t
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 102;
Best Local Similarity 95.5%; Pred. No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTGACAAAGTTGG 25
|||||

Db 35 CAGCTTTTGTGACAAAGTTGG 14
|||||

RESULT 33

CB399013/c

LOCUS CB399013 102 bp mRNA linear EST 15-MAY-2003

DEFINITION OSTR213H5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION OSTR213H5_1

VERSION CB399013.1 GI:30740740

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

REFERENCE Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditoidea

1 (bases 1 to 102)

Authors: Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevret, E., Papasotiropoulos, V., Tollas, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc_Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA=No.

Location/Qualifiers

1. .102

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 32 a 17 c 21 g 32 t
ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 102;
Best Local Similarity 95.5%; Pred. No. 9.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTGACAAAGTTGG 25
|||||

Db 46 CTGCTTTTGTGACAAAGTTGG 25
|||||

RESULT 34

CB396276/c

LOCUS CB396276 103 bp mRNA linear EST 15-MAY-2003

DEFINITION OSTR169D10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB396276

VERSION CB396276.1 GI:30737987

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

REFERENCE Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditoidea

1 (bases 1 to 103)

Authors: Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevret, E., Papasotiropoulos, V., Tollas, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc_Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA=No.

Location/Qualifiers

1. .103

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 29 a 25 c 17 g 32 t
ORIGIN

Query Match

Best Local Similarity 95.5%; Pred. No. 9.1e+02;

Query Match 81.6%; Score 20.4; DB 14; Length 103;

Best Local Similarity 95.5%; Pred. No. 9.1e+02;

/clone lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

BASE COUNT 24 a 22 c 20 g 32 t
 ORIGIN
 Query Match 81.6%; Score 20.4; DB 14; Length 98;
 Best Local Similarity 95.5%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 32 CAGCTTCTGTACAAAGTTGG 11

RESULT 28
 CB392051/c
 LOCUS 100 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF163A3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB392051
 VERSION CB392051.1 GI:30733761
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans

REFERENCE
 AUTHORS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 100)
 Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

TITLE
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

JOURNAL
 COMMENT Nat. Genet., (2003) In press
 Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david_hill@fci.harvard.edu or
 marc_vidal@fci.harvard.edu
 POLYA=No.

FEATURES
 source Location/Qualifiers
 1..100
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"
 BASE COUNT 32 a 24 c 18 g 26 t
 ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 100;
 Best Local Similarity 95.5%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 32 CAGCTTCTGTACAAAGTTGG 11

RESULT 29
 CB398867/c
 LOCUS 100 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR210H4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB398867
 VERSION CB398867.1 GI:30740594
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans

REFERENCE
 AUTHORS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 100)
 Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

TITLE
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

JOURNAL
 COMMENT Nat. Genet., (2003) In press
 Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david_hill@fci.harvard.edu or
 marc_vidal@fci.harvard.edu
 POLYA=No.

FEATURES
 source Location/Qualifiers
 1..100
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"
 BASE COUNT 34 a 22 c 18 g 26 t
 ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 100;
 Best Local Similarity 95.5%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 39 CTGCTTTTGTACAAAGTTGG 18

RESULT 30
 CB398991/c
 LOCUS 100 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR213C8_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB398991
 VERSION CB398991.1 GI:30740718

genome annotation and resource for proteome-scale protein

JOURNAL COMMENT

Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

FEATURES

source

Location/Qualifiers
1..95
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 28 a 20 c 19 g 28 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 95;
Best Local Similarity 95.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
|||||
DB 29 CAGCTTTCTGTGACAAAGTTGG 8

RESULT 26 CB401179/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB401179 97 bp mRNA linear EST 15-MAY-2003
OSTF190A5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB401179.1 GI:30742906
EST.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE AUTHORS

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu

TITLE

JOURNAL

COMMENT

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

FEATURES source

Location/Qualifiers
1..97
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 30 a 17 c 16 g 34 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 97;
Best Local Similarity 95.5%; Pred. No. 9.1e+02; 1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
|||||
DB 32 CAGCTTTCTGTGACAAAGTTGG 11

RESULT 27 CB402581/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB402581 98 bp mRNA linear EST 15-MAY-2003
OSTF215C2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB402581.1 GI:30744308
EST.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE AUTHORS

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu

JOURNAL COMMENT

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

FEATURES source

Location/Qualifiers
1..98
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"

```

QY      4  CAGCTTTTGTACAAAGTTGG 25
Db      32 CAGCTTCTTGTACAAAGTTGG 11

RESULT 23
CB402408/c
LOCUS   94 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF12B6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB402408
VERSION   CB402408.1 GI:307441135
KEYWORDS EST.
SOURCE   Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE
AUTHORS  Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
COMMENT  Contact: Vidal M
        Dana Farber Cancer Institute
        1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
        Tel: 617 632 5180
        Fax: 617 632 5739
        Email: Marc.Vidal@fci.harvard.edu
        Sequence tag of Gateway entry clones. The primers used were
        designed on the predicted protein encoding ORF. C. elegans ORFeome
        cloning project : Contact david_hill@fci.harvard.edu or
        marc_vidal@fci.harvard.edu
        POLYA=No.

FEATURES             Location/Qualifiers
     source          1..94
     /organism="Caenorhabditis elegans"
     /mol_type="mRNA"
     /strain="N2"
     /db_xref="taxon:6239"
     /sex="Hermaphrodite and male"
     /tissue_type="whole animal"
     /dev_stage="mixed stage"
     /clone_lib="AD-wrmcDNA"
     /note="The AD-wrmcDNA library was generated with poly(A) +
     RNA isolated from both hermaphrodite and male N2 worms of
     all larval stages, embryos, adults and dauers and the
     subsequent generation of cDNAs by poly(A) priming. The
     cDNAs were cloned into pPC86"

BASE COUNT  25 a  22 c  18 g  29 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 94;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4  CAGCTTTTGTACAAAGTTGG 25
Db      29 CAGCTTCTTGTACAAAGTTGG 8

RESULT 24
CB400591/c
LOCUS   95 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF179E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB400591
VERSION   CB400591.1 GI:30742318
KEYWORDS EST.
SOURCE   Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE
AUTHORS  Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
COMMENT  Contact: Vidal M
        Dana Farber Cancer Institute
        1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
        Tel: 617 632 5180
        Fax: 617 632 5739
        Email: Marc.Vidal@fci.harvard.edu
        Sequence tag of Gateway entry clones. The primers used were
        designed on the predicted protein encoding ORF. C. elegans ORFeome
        cloning project : Contact david_hill@fci.harvard.edu or
        marc_vidal@fci.harvard.edu
        POLYA=No.

FEATURES             Location/Qualifiers
     source          1..94
     /organism="Caenorhabditis elegans"
     /mol_type="mRNA"
     /strain="N2"
     /db_xref="taxon:6239"
     /sex="Hermaphrodite and male"
     /tissue_type="whole animal"
     /dev_stage="mixed stage"
     /clone_lib="AD-wrmcDNA"
     /note="The AD-wrmcDNA library was generated with poly(A) +
     RNA isolated from both hermaphrodite and male N2 worms of
     all larval stages, embryos, adults and dauers and the
     subsequent generation of cDNAs by poly(A) priming. The
     cDNAs were cloned into pPC86"

BASE COUNT  25 a  22 c  18 g  29 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 94;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

SOURCE
ORGANISM Caenorhabditis elegans
          Caenorhabditis elegans
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
          ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS  Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
COMMENT  Contact: Vidal M
        Dana Farber Cancer Institute
        1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
        Tel: 617 632 5180
        Fax: 617 632 5739
        Email: Marc.Vidal@fci.harvard.edu
        Sequence tag of Gateway entry clones. The primers used were
        designed on the predicted protein encoding ORF. C. elegans ORFeome
        cloning project : Contact david_hill@fci.harvard.edu or
        marc_vidal@fci.harvard.edu
        POLYA=No.

FEATURES             Location/Qualifiers
     source          1..95
     /organism="Caenorhabditis elegans"
     /mol_type="mRNA"
     /strain="N2"
     /db_xref="taxon:6239"
     /sex="Hermaphrodite and male"
     /tissue_type="whole animal"
     /dev_stage="mixed stage"
     /clone_lib="AD-wrmcDNA"
     /note="The AD-wrmcDNA library was generated with poly(A) +
     RNA isolated from both hermaphrodite and male N2 worms of
     all larval stages, embryos, adults and dauers and the
     subsequent generation of cDNAs by poly(A) priming. The
     cDNAs were cloned into pPC86"

BASE COUNT  39 a  16 c  16 g  24 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 95;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4  CAGCTTTTGTACAAAGTTGG 25
Db      29 CAGCTTCTTGTACAAAGTTGG 8

RESULT 25
CB401751/c
LOCUS   95 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF198G7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB401751
VERSION   CB401751.1 GI:30743478
KEYWORDS EST.
SOURCE   Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE
AUTHORS  Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet., (2003) In press
COMMENT  Contact: Vidal M
        Dana Farber Cancer Institute
        1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
        Tel: 617 632 5180
        Fax: 617 632 5739
        Email: Marc.Vidal@fci.harvard.edu
        Sequence tag of Gateway entry clones. The primers used were
        designed on the predicted protein encoding ORF. C. elegans ORFeome
        cloning project : Contact david_hill@fci.harvard.edu or
        marc_vidal@fci.harvard.edu
        POLYA=No.

FEATURES             Location/Qualifiers
     source          1..95
     /organism="Caenorhabditis elegans"
     /mol_type="mRNA"
     /strain="N2"
     /db_xref="taxon:6239"
     /sex="Hermaphrodite and male"
     /tissue_type="whole animal"
     /dev_stage="mixed stage"
     /clone_lib="AD-wrmcDNA"
     /note="The AD-wrmcDNA library was generated with poly(A) +
     RNA isolated from both hermaphrodite and male N2 worms of
     all larval stages, embryos, adults and dauers and the
     subsequent generation of cDNAs by poly(A) priming. The
     cDNAs were cloned into pPC86"

BASE COUNT  39 a  16 c  16 g  24 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 95;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```



```

marc.vidal@fci.harvard.edu
POLYA=No.

FEATURES
    source
        1..87
        /location/Qualifiers
        /organism="Caenorhabditis elegans"
        /mol_type="mRNA"
        /strain="N2"
        /db_xref="taxon:6239"
        /sex="Hermaphrodite and male"
        /tissue_type="whole animal"
        /dev_stage="mixed stage"
        /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
BASE COUNT      26 a 16 c 21 g 24 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 87;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
||||| ||||| ||||| |||||
Db 27 CAGCTTTCTGTACAAAGTTGG 6

RESULT 21
CB392047/c
LOCUS
DEFINITION
CB392047 90 bp mRNA linear EST 15-MAY-2003
ACCESSION
CB392047.1 GI:307333757
VERSION
CB392047.1
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 90)
AUTHORS
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.,
Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.

FEATURES
    source
        1..90
        /location/Qualifiers
        /organism="Caenorhabditis elegans"
        /mol_type="mRNA"
        /strain="N2"
        /db_xref="taxon:6239"
        /sex="Hermaphrodite and male"
        /tissue_type="whole animal"
        /dev_stage="mixed stage"
        /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
BASE COUNT      25 a 13 c 26 g 28 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 92;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25
||||| ||||| ||||| |||||
Db 31 CAGCTTTCTGTACAAAGTTGG 10

RESULT 22
CB402537/c
LOCUS
DEFINITION
CB402537 92 bp mRNA linear EST 15-MAY-2003
ACCESSION
CB402537.1 GI:30744264
VERSION
CB402537.1
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 92)
AUTHORS
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.,
Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet., (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.

FEATURES
    Location/Qualifiers
        1..92
        /organism="Caenorhabditis elegans"
        /mol_type="mRNA"
        /strain="N2"
        /db_xref="taxon:6239"
        /sex="Hermaphrodite and male"
        /tissue_type="whole animal"
        /dev_stage="mixed stage"
        /clone_lib="AD-wrmcDNA"
        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"
BASE COUNT      25 a 13 c 26 g 28 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 14; Length 92;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 633 GTTCAGCTTTTATANTAAAGTTGG 609

RESULT 18
CA986810/c
LOCUS
DEFINITION
CA986810 831 bp mRNA linear EST 06-JAN-2003
AGENCOURT 11113724 NICHDXGC Emb1 Xenopus laevis cDNA clone
IMAGE:6863318 5', mRNA sequence.
ACCESSION
CA986810.1 GI:27519481
VERSION
EST.
SOURCE
Xenopus laevis (African clawed frog)
ORGANISM
Xenopus laevis
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 831)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@emall.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1A14482 row: e column: 13
High quality sequence stop: 477.
Location/Qualifiers
1. .831
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6863318"
/tissue_type="embryo (stage 10)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHDXGC Emb1"
/notes="vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dt. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."
BASE COUNT 241 a 165 c 183 g 241 t 1 others
ORIGIN

FEATURES
source
Query Match 83.2%; Score 20.8; DB 14; Length 831;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTACGCTTTTGTACAAAGTTGG 25
    |||||
Db 821 TCCAGCTTTTGTACAAAGTTGG 798

RESULT 19
BX430288
LOCUS
DEFINITION
BX430288 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB0142D12 5-PRIME, mRNA sequence.
ACCESSION
BX430288
VERSION
BX430288.1 GI:30770931
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE002ZB04_AE00123_2&cluster=3874.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAE002ZB04_AE00123_2.
Location/Qualifiers
1. .868
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBB0142D12"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/notes="vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dt) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 193 a 230 c 170 g 274 t 1 others
ORIGIN

Query Match 83.2%; Score 20.8; DB 13; Length 868;
Best Local Similarity 91.7%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 599 TCCAGCTTTTGTACAAAGTTGG 622

RESULT 20
CB400039/c
LOCUS
DEFINITION
CB400039 87 bp mRNA linear EST 15-MAY-2003
OSTF167D8_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB400039
VERSION
CB400039.1 GI:30741766
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 87)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papatitropoulos, V., Tolia, P.P.
, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david.hill@dfci.harvard.edu or

```

```

COMMENT      Contact: ffrench-Constant RH
              Department of Biology and Biochemistry
              University of Bath
              South Building, Bath BA2 7AY, UK
              Tel: (44) 1225 826621
              Fax: (44) 1225 826779
              Email: bssrfc@bath.ac.uk
              This is one of 2,122 random reads from the M13 library. For
              annotation of identified clones (BLASTX, BLASTN and mapping to E.
              coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
              Acids Res.
              Seq primer: M13 Forward
              Class: shotgun.

FEATURES
  source
    Location/Qualifiers
      1..395
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /dev_stage="primary phase variant"
        /clone="PLG02205"
        /db_xref="taxon:29488"
        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /note="Genomic DNA from strain W14 was size selected (1-2
        kb) and then cloned into M13 Janus."
        kb) and then cloned into M13 Janus."
        Seq primer: M13 Forward
        Class: shotgun.

BASE COUNT   135 a 72 c 63 g 101 t 24 others
ORIGIN
  Query Match      83.2%; Score 20.8; DB 28; Length 395;
  Best Local Similarity 88.0%; Pred. No. 7.2e+02;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 210 GTTCAGCTTTTGTACAAAGTTGG 186

RESULT 17
AQ989566/c
LOCUS      AQ989566        664 bp    DNA    linear    GSS 14-AUG-2000
DEFINITION Photorhabdus luminescens strain W14 M13 library
            Photorhabdus luminescens genomic clone PLG01864, genomic survey
            sequence.
ACCESSION  AQ989566
VERSION    AQ989566.1 GI:9649605
KEYWORDS   GSS.
SOURCE     Photorhabdus luminescens
            Photorhabdus luminescens
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
REFERENCE  1 (bases 1 to 664)
            ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
            Daborn,P.J., Bowen,D. and Blattner,F.R.
            A genomic sample sequence of the entomopathogenic bacterium
            Photorhabdus luminescens W14: potential implications for virulence
            Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL    20378633
MEDLINE    20378633
PubMed     10919786
COMMENT    Contact: ffrench-Constant RH
            Department of Biology and Biochemistry
            University of Bath
            South Building, Bath BA2 7AY, UK
            Tel: (44) 1225 826621
            Fax: (44) 1225 826779
            Email: bssrfc@bath.ac.uk
            This is one of 2,122 random reads from the M13 library. For
            annotation of identified clones (BLASTX, BLASTN and mapping to E.
            coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
            Acids Res.
            Seq primer: M13 Forward
            Class: shotgun.

FEATURES
  source
    Location/Qualifiers
      1..751
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clone="PLG00126"
        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /note="Genomic DNA from strain W14 was size selected (1-2
        kb) and then cloned into M13 Janus."
        kb) and then cloned into M13 Janus."
        Seq primer: M13 Forward
        Class: shotgun.

BASE COUNT   217 a 159 c 171 g 200 t 4 others
ORIGIN
  Query Match      83.2%; Score 20.8; DB 28; Length 751;
  Best Local Similarity 88.0%; Pred. No. 7.7e+02;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 638 GTTCAGCTTTTGTACAAAGTTGG 614

RESULT 17
AQ989566/c
LOCUS      AQ989566        751 bp    DNA    linear    GSS 14-AUG-2000
DEFINITION Photorhabdus luminescens strain W14 M13 library
            Photorhabdus luminescens genomic clone PLG00126, genomic survey
            sequence.
ACCESSION  AQ989566
VERSION    AQ989566.1 GI:9648160
KEYWORDS   GSS.
SOURCE     Photorhabdus luminescens
            Photorhabdus luminescens
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
REFERENCE  1 (bases 1 to 751)
            ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
            Daborn,P.J., Bowen,D. and Blattner,F.R.
            A genomic sample sequence of the entomopathogenic bacterium
            Photorhabdus luminescens W14: potential implications for virulence
            Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL    20378633
MEDLINE    20378633
PubMed     10919786
COMMENT    Contact: ffrench-Constant RH
            Department of Biology and Biochemistry
            University of Bath
            South Building, Bath BA2 7AY, UK
            Tel: (44) 1225 826621
            Fax: (44) 1225 826779
            Email: bssrfc@bath.ac.uk
            This is one of 2,122 random reads from the M13 library. For
            annotation of identified clones (BLASTX, BLASTN and mapping to E.
            coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
            Acids Res.
            Seq primer: M13 Forward
            Class: shotgun.

FEATURES
  source
    Location/Qualifiers
      1..751
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clone="PLG00126"
        /dev_stage="primary phase variant"
        /clone_lib="Photorhabdus luminescens strain W14 M13
        library"
        /note="Genomic DNA from strain W14 was size selected (1-2
        kb) and then cloned into M13 Janus."
        kb) and then cloned into M13 Janus."
        Seq primer: M13 Forward
        Class: shotgun.

BASE COUNT   217 a 159 c 171 g 200 t 4 others
ORIGIN
  Query Match      83.2%; Score 20.8; DB 28; Length 751;
  Best Local Similarity 88.0%; Pred. No. 7.7e+02;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Query Match      87.2%; Score 21.8; DB 28; Length 743;
Best Local Similarity 92.0%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 626 GTTCAGCTTTTATATAAGTTGG 602

RESULT 13
AQ990110/c
LOCUS
DEFINITION
Rfc00827 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00827, genomic survey
sequence.
ACCESSION
AQ990110
VERSION
AQ990110.1 GI:9648704
KEYWORDS
GSS.
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 764)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..764
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
BASE COUNT 215 a 170 c 171 g 203 t 5 others
ORIGIN
Query Match      87.2%; Score 21.8; DB 28; Length 764;
Best Local Similarity 92.0%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 721 GTTCAGCTTTTATATAAGTTGG 697

RESULT 14
AQ990470/c
LOCUS
DEFINITION
Rfc01245 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01245, genomic survey
sequence.
ACCESSION
AQ990470
VERSION
AQ990470.1 GI:9649064
KEYWORDS
GSS.
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 769)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..769
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
BASE COUNT 223 a 163 c 174 g 204 t 5 others
ORIGIN
Query Match      87.2%; Score 21.8; DB 28; Length 769;
Best Local Similarity 92.0%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
    |||||
Db 631 GTTCAGCTTTTATATAAGTTGG 607

RESULT 15
AQ991303/c
LOCUS
DEFINITION
Rfc02205 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02205, genomic survey
sequence.
ACCESSION
AQ991303
VERSION
AQ991303.1 GI:9649897
KEYWORDS
GSS.
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 395)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
10919786

```


Query Match 87.2%; Score 21.8; DB 13; Length 472;
 Best Local Similarity 92.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 380 GTTCAGCTTTTATATACTAAGTTGG 356

RESULT 8
 BQ156404/c
 LOCUS
 DEFINITION NF092E031RUF1023 Irradiated Medicago truncatula cDNA clone
 ACCESSION BQ156404.1 GI:20293463
 VERSION BQ156404.1
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 473)
 REFERENCE
 AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
 Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula irradiated library
 COMMENT Unpublished
 Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 473 Std Error: 0.00
 Plate: 092 row: E column: 03
 Seq primer: TCACACAGGAACAGCTATGAC.
 Location/Qualifiers
 FEATURES
 source
 1..473
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /db_xref="taxon:3880"
 /clone="NF092E031R"
 /tissue_type="seedlings"
 /dev_stage="seedling"
 /clone_lib="irradiated"
 /note="Vector: Lambda Zap; Seedlings were exposed either
 to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
 Gamma-irradiated samples were harvested at 6, 12, 24 and
 48 hours after treatment. UV-irradiated samples were
 harvested 24 hours post-treatment. cDNA was prepared from
 polyA+ enriched, pooled samples of equivalent amounts of
 total RNA from each sample. The cDNA was directionally
 ligated into the Uni-Zap XR vector (stratagene) and
 packaged using the Gigapack III Gold packaging extracts.
 Phagemids containing cDNA inserts were in vivo excised
 from the recombinant Uni-Zap XR vector using ExAssist
 helper phage and the E. coli strain XL1-Blue MRF'
 (stratagene). Excised plasmids were plated using SOLR
 cells."

BASE COUNT 162 a 90 c 95 g 126 t
 ORIGIN

Query Match 87.2%; Score 21.8; DB 13; Length 473;
 Best Local Similarity 92.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 381 GTTCAGCTTTTATATACTAAGTTGG 357

RESULT 9
 B1422679/c
 LOCUS
 DEFINITION B1422679.1 5' end, mRNA sequence.
 ACCESSION B1422679
 VERSION B1422679.1 GI:15197297
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 597)
 REFERENCE
 AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
 Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning,
 C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 TITLE Generation of ESTs from tomato callus tissue
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html.
 Location/Qualifiers
 FEATURES
 source
 1..597
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEC71G2"
 /tissue_type="callus"
 /dev_stage="25-40 days old"
 /lab_host="XL1-Blue MRF"
 /clone_lib="tomato callus, TAMU"
 /note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Giovannoni laboratory; cDEC - Cotyledons
 of seedlings 7-10 days post-germination were excised, cut
 at both ends and placed on MS medium with no selection.
 Mixed callus was harvested at 25 and 40 days and included
 undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 193 a 109 c 131 g 164 t
 ORIGIN

Query Match 87.2%; Score 21.8; DB 12; Length 597;
 Best Local Similarity 92.0%; Pred. No. 3.1e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 552 GTTCAGCTTTTATATACTAAGTTGG 528

RESULT 10
 AQ991039/c
 LOCUS
 DEFINITION AQ991039.1 GI:9649633
 ACCESSION AQ991039
 VERSION AQ991039.1
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 1 (bases 1 to 695)
 REFERENCE
 AUTHORS french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 299)

REFERENCE
AUTHORS
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tonaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, D.M., Kanpin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazier, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirakawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
 Nature 420, 563-573 (2002)

MEDLINE
 22354683

PUBMED
 12466851

COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

FEATURES
 source
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 Location/Qualifiers
 1..229
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"

BASE COUNT 162 a 89 c 95 g 126 t
ORIGIN

/clone="I430040C03"
 /tissue type="whole body"
 /dev stage="18 days embryo"
 /clone lib="RIKEN full-length enriched, 18 days embryo whole body"
 85 a 50 c 54 g 110 t

BASE COUNT 85 a 50 c 54 g 110 t
ORIGIN

Query Match 87.2%; Score 21.8; DB 13; Length 299;
 Best Local Similarity 92.0%; Pred. No. 2.9e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 25
 |||||
Db 246 GTTCAGCTTTTGTACTAAGTTG 270

RESULT 7
 BQ157398/c
 BQ157398/1
 LOCUS
 DEFINITION
 BQ157398
 BQ157398
 BQ157398.1 GI:20294457
 EST.
 MEDICAGO truncatula (barrel medic)
 MEDICAGO truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 472)
 Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula irradiated library
 Unpublished
 Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 472 Std Error: 0.00
 Plate: 104 row: D column: 07
 Seq primer: TCACACAGGAAACAGCATGAC.
 Location/Qualifiers
 1..472
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /db_xref="taxon:3880"
 /clone="NF104D07IR"
 /tissue type="seedlings"
 /dev stage="seedling"
 /clone lib="irradiated"
 /note="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExSist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

Query Match 88.0%; Score 22; DB 14; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 41 CAGCTTTTGTACAAAGTTGG 20

RESULT 4
 CB388073/c

LOCUS CB388073 141 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTF091E12_1 AD-wrmCDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB388073
 VERSION CB388073.1 GI:30729783
 KEYWORDS EST.
 ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 141)
 AUTHORS ; Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Pelodetrinae; Caenorhabditis.
 Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
 , C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
 , J.R., Hartley, O.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P.,
 Ptacek, J.J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E., and Vidal, M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

TITLE C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

JOURNAL Nat. Genet., (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project; Contact david_hill@dfci.harvard.edu or
 marc_vidal@dfci.harvard.edu
 POLYA-No.

FEATURES
 source Location/Qualifiers
 1..141
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmCDNA"
 /note="The AD-wrmCDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"
 40 a 32 c 23 g 46 t

BASE COUNT 40 a 32 c 23 g 46 t
 ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 141;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 74 CAGCTTTTGTACAAAGTTGG 53

RESULT 5
 BQ156416/c

LOCUS BQ156416 206 bp mRNA linear EST 24-APR-2002
 DEFINITION NF092F02IRIF1027 Irradiated Medicago truncatula cDNA clone
 NF092F02IR 5', mRNA sequence.
 ACCESSION BQ156416
 VERSION BQ156416.1 GI:20293475
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 206)
 AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
 Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula irradiated library
 Unpublished
 COMMENT Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 206 Std Error: 0.00
 Plate: 092 row: F column: 02
 Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
 source Location/Qualifiers
 1..206
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /db_xref="taxon:3890"
 /clone="NF092F02IR"
 /tissue_type="seedlings"
 /dev_stage="seedling"
 /clone_lib="Irradiated"
 /note="Vector: Lambda Zap; Seedlings were exposed either
 to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
 Gamma-irradiated samples were harvested at 6, 12, 24 and
 48 hours after treatment. UV-irradiated samples were
 harvested 24 hours post-treatment. cDNA was prepared from
 polyA+ enriched, pooled samples of equivalent amounts of
 total RNA from each sample. The cDNA was directionally
 ligated into the Uni-Zap XR vector (Stratagene) and
 packaged using the Gigapack III Gold packaging extracts.
 Phagemids containing cDNA inserts were in vivo excised
 from the recombinant Uni-Zap XR vector using Exassist
 helper phage and the E. coli strain XL1-Blue MRF'
 (Stratagene). Excised plasmids were plated using SOUR
 cells."

BASE COUNT 81 a 27 c 39 g 59 t
 ORIGIN

Query Match 87.2%; Score 21.8; DB 13; Length 206;
 Best Local Similarity 92.0%; Pred. No. 2.8e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 167 GTTCAGCTTTTGTACAAAGTTGG 143

RESULT 6
 BY115594

LOCUS BY115594 299 bp mRNA linear EST 08-DEC-2002
 DEFINITION BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus
 musculus cDNA clone L430040C03 5', mRNA sequence.
 ACCESSION BY115594
 VERSION BY115594.1 GI:26226695
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Fax: 617 632 5739
 Email: Marc.Vidal@fci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@fci.harvard.edu or marc.vidal@fci.harvard.edu
 POLYA=No.

FEATURES

Location/Qualifiers

1..95
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

24 a 20 c 25 g 26 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25

Db 30 CAGCTTTTGTGACAAAGTTGG 9

RESULT 2

CB398919/c
 LOCUS 108 bp mRNA linear EST 15-MAY-2003

DEFINITION OSTR212B7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB398919

VERSION CB398919.1 GI:30740646

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Pelodierinae; Caenorhabditis.

1 (bases 1 to 108)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc.vidal@fci.harvard.edu

POLYA=No.

FEATURES

Location/Qualifiers

1..108
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"

BASE COUNT

41 a

ORIGIN

22 c 22 g 36 t

/db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT

27 a 23 c 18 g 40 t

ORIGIN

Query Match 88.0%; Score 22; DB 14; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGCTTTTGTGACAAAGTTGG 25

Db 45 CAGCTTTTGTGACAAAGTTGG 24

RESULT 3

CB392422/c

LOCUS 121 bp mRNA linear EST 15-MAY-2003

DEFINITION OSTR099E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB392422

VERSION CB392422.1 GI:30734133

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Pelodierinae; Caenorhabditis.

1 (bases 1 to 121)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong

, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson

, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,

Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P.

, Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet., (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc.vidal@fci.harvard.edu

POLYA=No.

FEATURES

Location/Qualifiers

1..121
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

BASE COUNT

41 a 22 c 22 g 36 t

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds
(without alignments)
555.531 Million cell updates/sec

Title: US-10-055-001A-10

Perfect score: 25
Sequence: 1 gttcagctttttgtacaaagtgg 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: em_estba:*
2: em_estum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_eston:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	88.0	95	14	CB402238
C 2	22	88.0	108	14	CB398919
C 3	22	88.0	121	14	CB392422
C 4	22	88.0	141	14	CB388073

C	5	21.8	87.2	206	13	BQ156416
C	6	21.8	87.2	299	13	BY115594
C	7	21.8	87.2	472	13	BQ157398
C	8	21.8	87.2	473	13	BQ156404
C	9	21.8	87.2	597	12	BI422679
C	10	21.8	87.2	695	28	AQ981039
C	11	21.8	87.2	712	28	AQ990809
C	12	21.8	87.2	743	28	AQ990346
C	13	21.8	87.2	764	28	AQ990110
C	14	21.8	87.2	769	28	AQ990470
C	15	20.8	83.2	395	28	AQ991303
C	16	20.8	83.2	664	28	AQ991011
C	17	20.8	83.2	751	28	AQ989566
C	18	20.8	83.2	831	14	CA986810
C	19	20.8	83.2	868	13	EX430288
C	20	20.4	81.6	87	14	CB400039
C	21	20.4	81.6	90	14	CB392047
C	22	20.4	81.6	92	14	CB402537
C	23	20.4	81.6	94	14	CB402408
C	24	20.4	81.6	95	14	CB400591
C	25	20.4	81.6	97	14	CB401179
C	26	20.4	81.6	98	14	CB402581
C	27	20.4	81.6	100	14	CB392051
C	28	20.4	81.6	100	14	CB398867
C	29	20.4	81.6	100	14	CB398991
C	30	20.4	81.6	100	14	CB400512
C	31	20.4	81.6	100	14	CB392040
C	32	20.4	81.6	102	14	CB399013
C	33	20.4	81.6	102	14	CB396276
C	34	20.4	81.6	103	14	CB401874
C	35	20.4	81.6	103	14	CB396275
C	36	20.4	81.6	106	14	CB396817
C	37	20.4	81.6	107	14	CB388456
C	38	20.4	81.6	111	14	CB394444
C	39	20.4	81.6	111	14	CB395510
C	40	20.4	81.6	112	14	CB396297
C	41	20.4	81.6	112	14	CB397516
C	42	20.4	81.6	112	14	CB398322
C	43	20.4	81.6	112	14	CB402012
C	44	20.4	81.6	114	14	CB396745
C	45	20.4	81.6	118	14	CB396745

ALIGNMENTS

RESULT 1
CB402238/c
LOCUS CB402238 95 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF209B3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB402238
VERSION CB402238.1 GI:30743965
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 95)
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brach, M.A., Vandenhaute, J., Boulton, S., Andres, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
Nat. Genet., (2003) In press
CONTACT: Vidal M

JOURNAL
COMMENT
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180

; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning

; FILE REFERENCE: 0942.5010002

; CURRENT APPLICATION NUMBER: US/09/732,914

; CURRENT FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 60/169,983

; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: US 60/188,020

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 10

; LENGTH: 27

; TYPE: DNA

; ORGANISM: attP2

US-09-732-914-10

Query Match 93.6%; Score 23.4; DB 9; Length 27;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

Search completed: November 7, 2003, 02:22:26
Job time : 102.25 secs

```
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
;           Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;           Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-162-879-16

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 38
US-10-161-403-51
; Sequence 51, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attP2,P3
US-10-161-403-56

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 39
US-10-161-403-56
; Sequence 56, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attP2,P3
US-10-161-403-56

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 40
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
```

```
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attR3
US-10-161-403-51
```

```
Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25
```

```
RESULT 39
US-10-161-403-56
; Sequence 56, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attP2,P3
US-10-161-403-56
```

```
Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25
```

```
RESULT 40
US-09-732-914-10
; Sequence 10, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
```

us-10-055-001a-10.rnpb

Fri Nov 7 08:08:37 2003

```

;
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-058-292-11

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   ||||||| ||||||| |||||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 35
US-10-058-292-16
; Sequence 16, Application US/10058292
; Publication No. US2003005452A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brach, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

US-10-058-292-16

```

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   ||||||| ||||||| |||||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 36
US-10-162-879-11
; Sequence 11, Application US/10162879
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brach, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-162-879-11

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   ||||||| ||||||| |||||||
Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

RESULT 37
US-10-162-879-16
; Sequence 16, Application US/10162879

```

us-10-055-001a-10.rnpb

Fri Nov 7 08:08:37 2003

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 31

US-10-300-892-16
; Sequence 16, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-16

Query Match 93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 32

US-10-055-001A-6
; Sequence 6, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attr3
US-10-055-001A-6

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 33

US-10-055-001A-11
; Sequence 11, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attr2,P3
US-10-055-001A-11

Query Match 93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 34

US-10-058-292-11
; Sequence 11, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002

```

RESULT 30
US-09-985-448-16
; Sequence 16, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-16

```

```
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-16

Query Match          93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 25
US-09-822-634-8
; Sequence 8, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
US-09-822-634-8

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 26
US-09-907-900-16
; Sequence 16, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
```

```
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-16

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 27
US-09-907-719-16
; Sequence 16, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-16

Query Match          93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 28
US-09-432-085-11
; Sequence 11, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
```



```

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-43

```

```

Query Match          95.2%; Score 23.8; DB 10; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.73;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

RESULT 21
US-09-907-719-43
; Sequence 43, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-43

```

```

Query Match          95.2%; Score 23.8; DB 10; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.73;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

RESULT 22
US-09-985-448-43
; Sequence 43, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

```

```

; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-43

```

```

Query Match          95.2%; Score 23.8; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.73;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

RESULT 23
US-10-300-892-43
; Sequence 43, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-43

```

```

Query Match          95.2%; Score 23.8; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.73;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

RESULT 24
US-09-855-797A-16
; Sequence 16, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.

```

Db 17792 GTTCAGCTTTTGTACAAAGTTGG 17816

RESULT 18

US-10-055-001A-13/c
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellmell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16835)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16351)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13

Query Match 100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.74; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 13146 GTTCAGCTTTTGTACAAAGTTGG 13122

RESULT 19

US-09-855-797A-43
; Sequence 43, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-855-797A-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 20

US-09-907-900-43
; Sequence 43, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.

us-10-055-001a-10.rnpb

Fri Nov 7 08:08:37 2003

```

; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match      100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.73; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 16963 GTTCAGCTTTTGTACAAAGTTGG 16987

RESULT 16
US-10-055-001A-23/c
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match      100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.73; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 13146 GTTCAGCTTTTGTACAAAGTTGG 13122

RESULT 17
US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-13

OTHER INFORMATION: acceptor vector pHELLSGATE4
FEATURE:
NAME/KEY: misc feature
LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
FEATURE:
NAME/KEY: misc feature
LOCATION: (10706)..(11324)
OTHER INFORMATION: right T-DNA border fragment
FEATURE:
NAME/KEY: misc feature
LOCATION: (11674)..(13019)
OTHER INFORMATION: CamV35S promoter fragment
FEATURE:
NAME/KEY: misc feature
LOCATION: (17890)..(17659)
OTHER INFORMATION: attP1 recombination site (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (17610)..(16855)
OTHER INFORMATION: ccdB selection marker (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron 2
FEATURE:
NAME/KEY: misc feature
LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
FEATURE:
NAME/KEY: misc feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
FEATURE:
NAME/KEY: misc feature
LOCATION: (13675)..(13980)
OTHER INFORMATION: ccdB selection marker (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attP1 recombination site
FEATURE:
NAME/KEY: misc feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase gene terminator region
FEATURE:
NAME/KEY: misc feature
LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
FEATURE:
NAME/KEY: misc feature
LOCATION: (497)..(1442)
OTHER INFORMATION: nptII coding region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
FEATURE:
NAME/KEY: misc feature
LOCATION: (2149)..(2706)
OTHER INFORMATION: a left T-DNA border region
US-10-055-001A-13

Query Match      100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.74; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25

```

```

, APPLICANT: Helliwell, Christopher A.
, TITLE OF INVENTION: Method and means for producing efficient silencing constructs
, TITLE OF INVENTION: using recombinational cloning
, FILE REFERENCE: HELLGA

```

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 9
US-10-162-879-15
; Sequence 15, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-10-162-879-15
Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 10
US-10-161-403-55
; Sequence 55, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attp1
; US-10-161-403-55

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 11
US-09-732-914-6
; Sequence 6, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: attp1
; US-09-732-914-6

Query Match 100.0%; Score 25; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 12
US-10-151-690-30

```
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-15

Query Match      100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 6
US-10-300-892-15
; Sequence 15, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-15

Query Match      100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 7
US-10-055-001A-10
; Sequence 10, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
```

```
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attp1
US-10-055-001A-10

Query Match      100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 8
US-10-058-292-15
; Sequence 15, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-058-292-15
```

US-09-907-900-15
; Sequence 15, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004 US/09/907,900
; CURRENT APPLICATION NUMBER: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-15

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 3

US-09-907-719-15
; Sequence 15, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-15

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 4

US-09-432-085-15

; Sequence 15, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-432-085-15

Query Match 100.0%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 5

US-09-985-448-15
; Sequence 15, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004

1	25	100.0	25	9	US-09-855-797A-15	Sequence 15, Appl
2	25	100.0	25	10	US-09-907-900-15	Sequence 15, Appl
3	25	100.0	25	10	US-09-907-719-15	Sequence 15, Appl
4	25	100.0	25	11	US-09-432-085-15	Sequence 15, Appl
5	25	100.0	25	12	US-09-985-448-15	Sequence 15, Appl
6	25	100.0	25	12	US-10-300-892-15	Sequence 15, Appl
7	25	100.0	25	14	US-10-055-001A-10	Sequence 10, Appl
8	25	100.0	25	14	US-10-058-292-15	Sequence 15, Appl
9	25	100.0	25	14	US-10-162-879-15	Sequence 15, Appl
10	25	100.0	25	14	US-10-161-403-55	Sequence 55, Appl
11	25	100.0	27	9	US-09-732-914-6	Sequence 6, Appl
12	25	100.0	27	14	US-10-151-690-30	Sequence 30, Appl
13	25	100.0	4470	14	US-10-151-690-21	Sequence 21, Appl
14	25	100.0	5584	14	US-10-151-690-61	Sequence 61, Appl
15	25	100.0	17862	14	US-10-055-001A-23	Sequence 23, Appl
16	25	100.0	17862	14	US-10-055-001A-23	Sequence 23, Appl

RESULT 2

RESULT 2


```

XX
SQ Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;
    Query Match 93.6%; Score 23.4; DB 25; Length 27;
    Best Local Similarity 96.0%; Pred. No. 1.2;
    Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAAGTTGG 25
   |||||||
Db 1 GTTCAGCTTTTGTACAAAAGTTGG 25

Search completed: November 6, 2003, 22:26:29
Job time : 111.5 secs

```

CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 25; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 39
 AAS06183
 ID AAS06183 standard; DNA; 27 BP.
 XX
 AC AAS06183;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Phage-lambda recombination site attP2.
 XX
 KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.
 XX
 OS Bacteriophage lambda.
 XX
 PN WO200142509-A1.
 XX
 PD 14-JUN-2001.
 XX
 PF 11-DEC-2000; 2000WO-US33546.
 XX
 PR 10-DEC-1999; 99US-0169983.
 PR 09-MAR-2000; 2000US-0188020.
 XX
 PA (CHEO/) CHEO D.
 PA (BRAS/) BRASCH M A.
 PA (TEMP/) TEMPLE G F.
 PA (HART/) HARTLEY J L.
 PA (BYRD/) BYRD D R N.

PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

DR WPI; 2001-356174/37.

XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one
 PT or more recombination sites in the presence of recombination proteins,
 PT e.g. Cre -

XX Disclosure; Fig 24A; 357pp; English.

XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination

CC site nucleic acid sequences, and PCR primers of the invention. The
 CC att sequences are recognised by the recombination protein lambda
 CC integrase (Int). The invention is a new method of producing a population
 CC of hybrid nucleic acids comprising mixing at least a first population of
 CC nucleic acids comprising one or more recombination sites with at least
 CC one target nucleic acid comprising one or more recombination sites and
 CC causing some or all of the nucleic acids to recombine with all or some of
 CC the target nucleic acids. The method is useful for producing a population
 CC of hybrid nucleic acids which may be the same or different. The nucleic
 CC acids may be used to express therapeutic proteins or peptides and they
 CC may also be used to create novel fusion proteins by expressing different
 CC sequences linked to each other. The method allows simultaneous cloning of
 CC two or more different nucleic acids.

XX Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 22; Length 27;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 40
 ABZ58736
 ID ABZ58736 standard; DNA; 27 BP.
 XX
 AC ABZ58736;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE Att site nucleotide sequence attP2.
 XX
 KW Nucleic acid insertion; recombination; nucleic acid selection;
 KW nucleic acid isolation; att; ds.
 XX
 OS Synthetic.
 XX
 PN WO200295055-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 21-MAY-2002; 2002WO-US15947.
 XX
 PR 21-MAY-2001; 2001US-291973P.
 XX
 PA (INVI-) INVITROGEN CORP.

PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

DR WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule
 PT for selecting and isolating nucleic acid molecules by mixing the second
 PT population of nucleic acid with a second target nucleic acid -

PS Disclosure; Fig 13A; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
 CC second target molecule. The method involves (a) mixing a first population
 CC of nucleic acid comprising one or more recombination sites with a target
 CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
 CC the first population to recombine with the first target nucleic acid
 CC molecules to form a second population; (c) mixing the second population
 CC of nucleic acid with a second target nucleic acid; and (d) causing some
 CC or all of the nucleic acid molecules of the second population to
 CC recombine with some or all of the second target nucleic acid molecules to
 CC form a third population of nucleic acid. The method is useful for
 CC selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
 CC represent att recombination site sequences used in the method of the
 CC invention.

PT interest -
 PS Claim 43; Page 143; 272pp; English.
 XX
 CC The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (1) a platform artificial chromosome
 CC expression system (ACes) (II) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (II) is useful for producing a
 CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 25; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 37
 ABT16630
 ID ABT16630 standard; DNA; 25 BP.
 XX
 AC ABT16630;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Artificial plant chromosome related oligo SEQ ID No 42.
 XX
 KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
 KW blood factor; herbicide; stress; agronomical; nutrient quality;
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.
 XX
 OS Unidentified.
 XX
 PN WO200296923-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-US17451.
 XX
 PR 30-MAY-2001; 2001US-294687P.
 PR 04-JUN-2001; 2001US-296329P.
 XX
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 PI Perez C, Fabijanski SF, Perkins E;
 XX
 DR WPI; 2003-140436/13.
 XX
 PT Producing artificial chromosome by introducing a nucleic acid into
 PT plant cell, selecting artificial chromosome that has one or more repeat
 PT regions with equivalent amounts of euchromatic and heterochromatic
 PT nucleic acids -
 XX
 PS Disclosure; Page 263; 269pp; English.

PS Disclosure; Page 263; 269pp; English.
 XX
 CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, cRNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, blood factors, antigens, hormones,
 CC biopharmaceutical proteins, vaccines, antibodies, or a product that provides for
 CC cytokines, growth factors, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 25; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 38
 ABT16635
 ID ABT16635 standard; DNA; 25 BP.
 XX
 AC ABT16635;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Artificial plant chromosome related oligo SEQ ID No 47.
 XX
 KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
 KW blood factor; herbicide; stress; agronomical; nutrient quality;
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.
 XX
 OS Unidentified.
 XX
 PN WO200296923-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-US17451.
 XX
 PR 30-MAY-2001; 2001US-294687P.
 PR 04-JUN-2001; 2001US-296329P.
 XX
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 PI Perez C, Fabijanski SF, Perkins E;
 XX
 DR WPI; 2003-140436/13.
 XX
 PT Producing artificial chromosome by introducing a nucleic acid into
 PT plant cell, selecting artificial chromosome that has one or more repeat
 PT regions with equivalent amounts of euchromatic and heterochromatic
 PT nucleic acids -
 XX
 PS Disclosure; Page 263; 269pp; English.

PT of replication, a selectable marker and a chimeric DNA construct,
 PT useful for silencing target nucleic acids and for producing large
 PT amounts of double-stranded RNA -

XX
 XX
 PS Claim 12; Page 15; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked
 CC DNA fragments having: (a) origin of replication allowing replication in a
 CC recipient cell, preferably in bacteria such as *Escherichia coli*;
 CC (b) selectable marker region capable of being expressed in the recipient
 CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
 CC promoter region capable of being recognized by RNA polymerases of a
 CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
 CC third and fourth recombination sites; (iii) 3' transcription terminating
 CC and polyadenylation region functional in the eukaryotic cell. The first
 CC and fourth recombination sites, or the second and third recombination
 CC sites are capable of reacting with a same recombination site, and
 CC preferably are identical. The first and second recombination sites, or
 CC the third and fourth recombination sites, do not recombine with each
 CC other or with a same recombination site. The vector is useful for
 CC producing large amounts of double-stranded RNA which can be used for
 CC silencing target nucleic acid sequences. The vectors can also be used to
 CC convert a DNA fragment into an inverted repeat structure. Plants
 CC transformed with a vector from the present invention can be used in a
 CC conventional breeding scheme to produce more plants with the same
 CC characteristics or to introduce a chimeric gene for reduction of the
 CC phenotypic expression of nucleic acids. The present sequence represents
 CC the core sequence of recombination site attB1 which is given in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

SQ Query Match 93.6%; Score 23.4; DB 24; Length 25;

Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 35

ACC44660
 ID ACC44660 standard; DNA; 25 BP.

XX
 AC ACC44660;

XX 29-MAY-2003 (first entry)

DE Recombination site related oligonucleotide SEQ ID NO:51.

XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
 KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
 KW platform artificial chromosome expression system; PCR primer; ss.

OS Synthetic.

PN WO200297059-A2.

PD 05-DEC-2002.

XX 30-MAY-2002; 2002WO-US17452.

PF 30-MAY-2001; 2001US-294758P.

PR 21-MAR-2002; 2002US-366891P.

XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 PI Stewart S, Shellard J;

XX WPI; 2003-140461/13.

XX

PT Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT interest -

XX Claim 43; Page 143; 272pp; English.

XX The present invention describes a eukaryotic chromosome (I) comprising
 CC one or several att sites, where an att site is heterologous to the
 CC chromosome, and permits site-directed integration in the presence of
 CC lambda-integrase. Also described: (i) a platform artificial chromosome
 CC expression system (ACes) (ii) comprising several sites that participate
 CC in recombinase catalysed recombination; and (2) a method (M1) for
 CC introducing a heterologous nucleic acid into a platform artificial
 CC chromosome. (I) can be used in gene therapy. (M1) is useful for
 CC introducing a heterologous nucleic acid molecule into a platform
 CC artificial chromosome, preferably an ACes. (ii) is useful for producing a
 CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
 CC mammal) by introducing (ii) by cell fusion, lipid-mediated transfection
 CC by a carrier system, microinjection, microcell fusion, electroporation,
 CC microprojectile bombardment or direct DNA transfer into an embryonic
 CC cell, preferably a stem cell or an embryo. (ii) comprises a heterologous
 CC nucleic acid that encodes a therapeutic product which is useful for
 CC making a library of ACes comprising random portions of a genome. ACC44612
 CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

SQ Query Match 93.6%; Score 23.4; DB 25; Length 25;

Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 36

ACC44665

ID ACC44665 standard; DNA; 25 BP.

XX ACC44665;

XX 29-MAY-2003 (first entry)

XX Recombination site related oligonucleotide SEQ ID NO:56.

XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
 KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
 KW platform artificial chromosome expression system; PCR primer; ss.

OS Synthetic.

PN WO200297059-A2.

XX 05-DEC-2002.

XX 30-MAY-2002; 2002WO-US17452.

XX 30-MAY-2001; 2001US-294758P.

PR 21-MAR-2002; 2002US-366891P.

XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
 PI Stewart S, Shellard J;

XX WPI; 2003-140461/13.

XX Novel eukaryotic chromosome comprising one or many att sites which
 PT permits site-directed integration in the presence of lambda-integrase,
 PT useful for site-specific recombination-directed integration of DNA of
 PT

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PI Vile RG, Harrington K, Murphy S, Bateman A;
XX WPI; 2001-656985/75.
XX
XX Recombinant nucleic acid vector for reducing tumour size, has expression
PT cassette comprises a promoter linked to nucleic acid sequence encoding
PT a syncytium-inducing polypeptide and flanked on either side by
PT recombinase -
XX
XX
XX Disclosure; Page 42; 84pp; English.
XX
XX The invention relates to a recombinant nucleic acid vector comprising a
CC first expression cassette, comprising a first promoter operably linked to
CC a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
CC as a fusogenic membrane glycoprotein) and flanked on either side by a
CC sequence recognised by a recombinase, and/or a second expression cassette
CC comprising a tumour-specific promoter operably linked to a nucleic acid
CC sequence encoding a recombinase. The nucleic acid of the first expression
CC cassette may be linked to a hypoxic response element (HRE), the second
CC expression cassette may contain a promoter linked to a nucleic acid
CC encoding a cytokine, and a third cassette may contain a tumour specific
CC promoter linked to the nucleic acid encoding the recombinase. The tumour
CC specific promoter is, for example, a carcinoembryonic antigen (CEA)
CC promoter or a tyrosinase promoter and the recombinase is, for example,
CC Cre recombinase or FLP recombinase. The invention is useful for reducing
CC tumour size by administering the compositions as retroviral vectors, or
CC in a cell containing the vector, to an individual in need of treatment
CC for a disease caused by malignant cells. This sequence represents an Int
CC recombinase site core region attR3, required for excisive recombination.
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
SQ
Query Match 93.6%; Score 23.4; DB 23; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
DB 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
RESULT 33
ABQ82123
ID ABQ82123 standard; DNA; 25 BP.
XX
XX ABQ82123;
XX
XX 11-DEC-2002 (first entry)
DE Core sequence of recombination site attR3 SEQ ID NO:6.
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ss.
XX
XX Synthetic.
XX WO200259294-A1.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU00073.
XX
XX 26-JAN-2001; 2001US-264067P.
XX
XX 29-NOV-2001; 2001US-333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin

PT New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX
XX Disclosure; Page 15; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerases of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC the core sequence of recombination site attB1 which is given in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
SQ
Query Match 93.6%; Score 23.4; DB 24; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
DB 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
RESULT 34
ABQ82128
ID ABQ82128 standard; DNA; 25 BP.
XX
XX ABQ82128;
XX
XX 11-DEC-2002 (first entry)
DE Core sequence of recombination site attP2,P3 SEQ ID NO:11.
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ss.
XX
XX Synthetic.
XX WO200259294-A1.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU00073.
XX
XX 26-JAN-2001; 2001US-264067P.
XX
XX 29-NOV-2001; 2001US-333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin


```

CC useful for recombination cloning.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match          93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 28
AAF55745
ID AAF55745 standard; DNA; 25 BP.
XX
AC AAF55745;
XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attr3.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.
XX
PN US6171861-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JAN-1998; 98US-0005476.
XX
PR 07-JUN-1996; 96US-0663002.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX
OS Unidentified.
XX
PN US6171861-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JAN-1998; 98US-0005476.
XX
PR 07-JUN-1996; 96US-0663002.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2001-136877/14.
XX
PT In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host -
XX
PS Claim 25; Column 46; 73pp; English.
XX
CC The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match          93.6%; Score 23.4; DB 22; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 30
AAC87876
ID AAC87876 standard; DNA; 25 BP.
XX
AC AAC87876;
XX
DT 02-MAR-2001 (first entry)
XX
DE Escherichia coli core region recombinant site attr3 SEQ ID NO:11.
XX
KW Core region; recombination site; cloning; chimeric DNA;
KW characteristic; mutation; att site; lox site; ss.
XX
OS Escherichia coli.
XX

```

DR WPI; 1999-303011/25.
 XX New nucleic acid cloning methods
 PT Disclosure; Page 163; 185pp; English.
 PS The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
 CC or more desired nucleic acid segments flanked by at least 2
 CC recombination sites which do not recombine with each other; (2) one or
 CC more vector donor molecules (VDMs) comprising at least 2 recombination
 CC sites which do not recombine with each other; and (3) one or more
 CC site-specific recombination proteins; (b) incubating the combination to
 CC transfer one or more of the desired segments into one or more of the
 CC VDMs, thereby producing one or more desired product molecules (PMs). The
 CC methods can be used for the efficient and specific recombination of NAM
 CC segments. They can be used to generate chimeric DNA or RNA molecules that
 CC have the desired characteristics and/or nucleic acid segments. The
 CC methods can also be used for changing vectors. The oligonucleotides
 CC AAX78935-X78994 are used in the method of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 20; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 26
 AAD14439
 ID AAD14439 standard; DNA; 25 BP.
 AC AAD14439;
 XX 01-NOV-2001 (first entry)
 DT Recombination site attR3 DNA.
 DE Recombination site; copy number; replicon; recombinatorial cloning;
 XX attR3; ds.
 KW Unidentified.
 OS US6270969-B1.
 XX 07-AUG-2001.
 XX 20-JAN-1999; 99US-0233492.
 XX 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX (INVI-) INVITROGEN CORP.
 PA Hartley JL, Brasch MA;
 PI WPI; 2001-488248/53.
 DR Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 XX Claim 14; Column 18; 76pp; English.
 PS The invention relates to a method for apposing an expression signal and
 XX a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 PT partial gene in the presence of a recombination protein under conditions
 PT sufficient to cause recombination and therefore appose the expression
 PT signal and the gene or partial gene. The methods are useful for apposing
 PT an expression signal and a gene or partial gene using recombinatorial
 XX cloning. The methods are also useful for changing vectors, constructing
 XX genes for fusion proteins, changing copy number, changing replicons,
 XX cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site

CC partial gene in the presence of a recombination protein under conditions
 CC sufficient to cause recombination and therefore appose the expression
 CC signal and the gene or partial gene. The methods are useful for apposing
 CC an expression signal and a gene or partial gene using recombinatorial
 CC cloning. The methods are also useful for changing vectors, constructing
 CC genes for fusion proteins, changing copy number, changing replicons,
 CC cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
 Query Match 93.6%; Score 23.4; DB 22; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.2;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 27
 AAD14444
 ID AAD14444 standard; DNA; 25 BP.
 AC AAD14444;
 XX 01-NOV-2001 (first entry)
 DT Recombination site attP2,P3 DNA.
 DE Recombination site; copy number; replicon; recombinatorial cloning;
 XX attP2,P3; ds.
 KW Unidentified.
 OS US6270969-B1.
 XX 07-AUG-2001.
 XX 20-JAN-1999; 99US-0233492.
 XX 07-JUN-1996; 96US-0663002.
 PR 07-JUN-1995; 95US-0486139.
 XX (INVI-) INVITROGEN CORP.
 PA Hartley JL, Brasch MA;
 PI WPI; 2001-488248/53.
 DR Methods for apposing nucleic acids comprising an expression signal and
 PT a gene/partial gene, using recombinatorial cloning by incubating the
 PT nucleic acids in the presence of a recombination protein under
 PT conditions for recombination -
 XX Claim 14; Column 18; 76pp; English.
 PS The invention relates to a method for apposing an expression signal and
 XX a gene or partial gene, using recombinatorial cloning. The method
 CC incubates nucleic acids comprising the expression signal and the gene/
 PT partial gene in the presence of a recombination protein under conditions
 PT sufficient to cause recombination and therefore appose the expression
 PT signal and the gene or partial gene. The methods are useful for apposing
 PT an expression signal and a gene or partial gene using recombinatorial
 XX cloning. The methods are also useful for changing vectors, constructing
 XX genes for fusion proteins, changing copy number, changing replicons,
 XX cloning into phages, and cloning e.g., PCR products (with an attB site
 CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
 CC The methods are highly specific, rapid, and less labour intensive than
 CC prior art methods. The present sequence is a recombination site


```

RESULT 23
AAx78977
ID AAX78977 standard; DNA; 25 BP.
XX
AC AAX78977;
XX
DT 17-AUG-1999 (first entry)
XX
DE Oligonucleotide #43 for recombination and cloning method.
XX
KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
OS Synthetic.
XX
PN WO9921977-A1.
XX
PD 06-MAY-1999.
XX
PF 26-OCT-1998; 98WO-US22589.
XX
PR 23-OCT-1998; 98US-0177387.
XX
PR 24-OCT-1997; 97US-0065930.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Fox DK, Hartley JL, Temple GF;
XX
XX WPI; 1999-303011/25.
XX
PT New nucleic acid cloning methods
XX
PS Disclosure; Page 171; 185pp; English.
XX
CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more
CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that
CC have the desired characteristics and/or nucleic acid segments. The
CC methods can also be used for changing vectors. The oligonucleotides
CC AAX78935-X78994 are used in the method of the invention.
XX
SQ Sequence 25 BP; 4 A; 3 C; 5 G; 10 T; 3 other;

Query Match 95.2%; Score 23.8; DB 20; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.81;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTGTACAAAGTTGG 25

RESULT 24
AAT48225
ID AAT48225 standard; DNA; 25 BP.
XX
AC AAT48225;
XX
DT 20-OCT-1997 (first entry)
XX
DE attp2,P3 core region.
XX
KW att recombination site; core region; mutation; enhance; recombination;
XX vector; subcloning; regulation; exchange; ss.
XX

```

```

OS Synthetic.
XX WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US10082.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
XX WPI; 1997-065168/06.
XX
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in
PT vitro or in vivo
XX
PS Claim 14; Page 56; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 18; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTGTACAAAGTTGG 25

RESULT 25
AAX78950
ID AAX78950 standard; DNA; 25 BP.
XX
AC AAX78950;
XX
DT 17-AUG-1999 (first entry)
XX
DE Oligonucleotide #16 for recombination and cloning method.
XX
KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
OS Synthetic.
XX
XX WO9921977-A1.
XX
PD 06-MAY-1999.
XX
PF 26-OCT-1998; 98WO-US22589.
XX
PR 23-OCT-1998; 98US-0177387.
XX
PR 24-OCT-1997; 97US-0065930.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Fox DK, Hartley JL, Temple GF;
XX
XX

```

Db 5458 GTTCAGCTTTTGTACAAAGTTGG 5482
|||||

RESULT 21
ABQ82130
ID ABQ82130 standard; DNA; 18691 BP.
XX AC ABQ82130;
XX DT 11-DEC-2002 (first entry)
XX DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.
XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KM recombination site; double stranded RNA; plant; ds.
XX OS Synthetic.
XX PN WO200259294-A1.
XX PD 01-AUG-2002.
XX PF 24-JAN-2002; 2002WO-AU00073.
XX PR 26-JAN-2001; 2001US-264067P.
XX PR 29-NOV-2001; 2001US-333743P.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PI Wesley S, Waterhouse P, Helliwell C;
XX DR WPI; 2002-682669/73.
XX PT New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX PS Claim 13; Page 62-72; 104pp; English.

XX CC The present invention describes a vector (I) comprising operably linked
XX CC DNA fragments having: (a) origin of replication allowing replication in a
XX CC recipient cell, preferably in bacteria such as Escherichia coli;
XX CC (b) selectable marker region capable of being expressed in the recipient
XX CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX CC promoter region capable of being recognized by RNA polymerases of a
XX CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX CC third and fourth recombination sites; (iii) 3' transcription terminating
XX CC and polyadenylation region functional in the eukaryotic cell. The first
XX CC sites are capable of reacting with a same recombination site, and
XX CC the third and fourth recombination sites, do not recombine with each
XX CC other or with a same recombination site. The vector is useful for
XX CC producing large amounts of double-stranded RNA which can be used to
XX CC silence target nucleic acid sequences. The vectors can also be used to
XX CC convert a DNA fragment into an inverted repeat structure. Plants
XX CC transformed with a vector from the present invention can be used in a
XX CC conventional breeding scheme to produce more plants with the same
XX CC characteristics or to introduce a chimeric gene for reduction of the
XX CC phenotypic expression of nucleic acids. The present sequence represents
XX CC an acceptor vector nucleotide sequence from the present invention.

SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

Db 17792 GTTCAGCTTTTGTACAAAGTTGG 17816
|||||

RESULT 22
ABQ82130/c
ID ABQ82130 standard; DNA; 18691 BP.
XX AC ABQ82130;
XX DT 11-DEC-2002 (first entry)
XX DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.
XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KM recombination site; double stranded RNA; plant; ds.
XX OS Synthetic.
XX PN WO200259294-A1.
XX PD 01-AUG-2002.
XX PF 24-JAN-2002; 2002WO-AU00073.
XX PR 26-JAN-2001; 2001US-264067P.
XX PR 29-NOV-2001; 2001US-333743P.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PI Wesley S, Waterhouse P, Helliwell C;
XX DR WPI; 2002-682669/73.
XX PT New vectors comprising operably linked DNA fragments having an origin
PT of replication, a selectable marker and a chimeric DNA construct,
PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX PS Claim 13; Page 62-72; 104pp; English.

XX CC The present invention describes a vector (I) comprising operably linked
XX CC DNA fragments having: (a) origin of replication allowing replication in a
XX CC recipient cell, preferably in bacteria such as Escherichia coli;
XX CC (b) selectable marker region capable of being expressed in the recipient
XX CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX CC promoter region capable of being recognized by RNA polymerases of a
XX CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX CC third and fourth recombination sites; (iii) 3' transcription terminating
XX CC and polyadenylation region functional in the eukaryotic cell. The first
XX CC sites are capable of reacting with a same recombination site, and
XX CC the third and fourth recombination sites, do not recombine with each
XX CC other or with a same recombination site. The vector is useful for
XX CC producing large amounts of double-stranded RNA which can be used to
XX CC silence target nucleic acid sequences. The vectors can also be used to
XX CC convert a DNA fragment into an inverted repeat structure. Plants
XX CC transformed with a vector from the present invention can be used in a
XX CC conventional breeding scheme to produce more plants with the same
XX CC characteristics or to introduce a chimeric gene for reduction of the
XX CC phenotypic expression of nucleic acids. The present sequence represents
XX CC an acceptor vector nucleotide sequence from the present invention.

SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

Db 13146 GTTCAGCTTTTGTACAAAGTTGG 13122
|||||

CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX

SQ Sequence 5156 BP; 1413 A; 1183 C; 1216 G; 1342 T; 2 other;

Query Match 100.0%; Score 25; DB 21; Length 5156;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||
Db 212 GTTCAGCTTTTGTACAAAGTTGG 236
|||

RESULT 19

AAC55632
ID AAC55632 standard; DNA; 5584 BP.

AC AAC55632;

DT 11-JAN-2001 (first entry)

XX Donor plasmid pDONR207 nucleotide sequence.

DE Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

PN WO200052027-A1.

XX 08-SEP-2000.

PF 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -

XX Disclosure; Fig 97; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (i) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from

CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX

SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.39; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||
Db 5458 GTTCAGCTTTTGTACAAAGTTGG 5482
|||

RESULT 20

ABZ58766

ID ABZ58766 standard; DNA; 5584 BP.

AC ABZ58766;

DT 01-MAY-2003 (first entry)

XX Donor plasmid pDONR207 nucleotide sequence.

DE Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.

XX Synthetic.

PN WO200295055-A2.

XX 28-NOV-2002.

PF 21-MAY-2002; 2002WO-US15947.

PR 21-MAY-2001; 2001US-291973P.

XX (INVI-) INVITROGEN CORP.

PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DR;

DR WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -

XX Disclosure; Fig 18B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence.

SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.39; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

CC of nucleic acid with a second target nucleic acid; and (d) causing some
 CC or all of the nucleic acid molecules of the second population to
 CC recombine with some or all of the second target nucleic acid molecules to
 CC form a third population of nucleic acid. The method is useful for
 CC selecting and isolating nucleic acid molecules. The present sequence
 CC represents the destination plasmid pDONR201 nucleotide sequence.

XX
 SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
 Query Match 100.0%; Score 25; DB 25; Length 4470;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 127 GTTCAGCTTTTGTACAAAGTTGG 103

RESULT 17
 AAC5525/c
 ID AAC5525 standard; DNA; 4939 BP.
 XX
 AC AAC5525;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Donor plasmid pDONR205 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 10; Fig 53; 459pp; English.

XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from

CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 other;
 Query Match 100.0%; Score 25; DB 21; Length 4939;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 3661 GTTCAGCTTTTGTACAAAGTTGG 3637

RESULT 18
 AAC5526
 ID AAC5526 standard; DNA; 5156 BP.
 XX
 AC AAC5526;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Donor plasmid pDONR206 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 9; Fig 54; 459pp; English.

XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 4208 BP; 1172 A; 997 C; 875 G; 1164 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4208;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 3283 GTTCAGCTTTTGTACAAAGTTGG 3259

RESULT 15
 AAC5521/c
 ID AAC55521 standard; DNA; 4470 BP.

AC AAC55521;
 DT 11-JAN-2001 (first entry)
 DE Donor plasmid pDONR201 nucleotide sequence.

KW Bacteriophage lambda: att; recombination site; attB, attP, attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW Gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
 OS Synthetic.

PN WO200052027-A1.

PD 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

PR 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 9; Fig 49; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4470;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 127 GTTCAGCTTTTGTACAAAGTTGG 103

RESULT 16
 ABZ58767/c
 ID ABZ58767 standard; DNA; 4470 BP.

AC ABZ58767;

DT 01-MAY-2003 (first entry)

DE Destination plasmid pDONR201 nucleotide sequence.

KW Nucleic acid insertion; recombination; nucleic acid selection;
 KW nucleic acid isolation; ds.

XX Synthetic.

XX WO200295055-A2.

PD 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US15947.

XX 21-MAY-2001; 2001US-291973P.

XX (INVI-) INVITROGEN CORP.

PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule
 PT for selecting and isolating nucleic acid molecules by mixing the second
 PT population of nucleic acid with a second target nucleic acid -

XX Disclosure; Fig 26B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
 CC second target molecule. The method involves (a) mixing a first population
 CC of nucleic acid comprising one or more recombination sites with a target
 CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
 CC the first population to recombine with the first target nucleic acid
 CC molecules to form a second population; (c) mixing the second population

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 1 other;

Query Match 100.0%; Score 25; DB 21; Length 4165;
 Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 212 GTTCAGCTTTTGTACAAAGTTGG 236

RESULT 13
 AAC55522
 ID AAC55522 standard; DNA; 4204 BP.
 XX
 AC AAC55522;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Donor plasmid pDONR202 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 9; Fig 50; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 4204 BP; 1198 A; 912 C; 959 G; 1135 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4204;
 Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 260 GTTCAGCTTTTGTACAAAGTTGG 284

RESULT 14
 AAC55523/C
 ID AAC55523 standard; DNA; 4208 BP.
 XX
 AC AAC55523;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Donor plasmid pDONR203 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 9; Fig 51; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

DR WPI; 2003-129436/12.
 XX Inserting a population of nucleic acids into a second target molecule
 PT for selecting and isolating nucleic acid molecules by mixing the second
 PT population of nucleic acid with a second target nucleic acid -
 XX
 PS Disclosure; Fig 13A; 273pp; English.
 XX
 CC The invention relates to inserting a population of nucleic acids into a
 CC second target molecule. The method involves (a) mixing a first population
 CC of nucleic acid comprising one or more recombination sites with a target
 CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
 CC the first population to recombine with the first target nucleic acid
 CC molecules to form a second population; (c) mixing the second population
 CC of nucleic acid with a second target nucleic acid; and (d) causing some
 CC or all of the nucleic acid molecules of the second population to
 CC recombine with some or all of the second target nucleic acid molecules to
 CC form a third population of nucleic acid. The method is useful for
 CC selecting and isolating nucleic acid molecules. Sequences AB258727-762
 CC represent att recombination site sequences used in the method of the
 CC invention.
 XX
 SQ Sequence 27 BP; 6 A; 4 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 11
 AAC55382
 ID AAC55382 standard; DNA; 233 BP.
 XX
 AC AAC55382;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Recombination site nucleotide sequence attP1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Claim 1; Fig 9; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (i), (ii), (iii), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 233 BP; 73 A; 32 C; 34 G; 94 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 233;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 Db 134 GTTCAGCTTTTGTACAAAGTTGG 158

RESULT 12
 AAC55524
 ID AAC55524 standard; DNA; 4165 BP.
 XX
 AC AAC55524;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Donor plasmid pDONR204 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 9; Fig 52; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

PD 05-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-US17451.
 XX
 PR 30-MAY-2001; 2001US-294687P.
 PR 04-JUN-2001; 2001US-296329P.
 XX
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 PI Perez C, Fabijanski SF, Perkins E;
 XX
 XX WPI; 2003-140436/13.
 DR
 XX
 PT Producing artificial chromosome by introducing a nucleic acid into
 PT plant cell, selecting artificial chromosome that has one or more repeat
 PT regions with equivalent amounts of euchromatic and heterochromatic
 PT nucleic acids -
 XX
 XX Disclosure; Page 263; 269pp; English.
 PS
 XX The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 9
 AAS06179
 ID AAS06179 standard; DNA; 27 BP.
 AC
 AC AAS06179;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 XX Phase-lambda recombination site attP1.
 DE
 DE Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.
 KW
 OS Bacteriophage lambda.
 OS
 XX WO200142509-A1.
 PN
 XX 14-JUN-2001.
 XX
 PD 11-DEC-2000; 2000WO-US33546.
 PF
 XX

PR 10-DEC-1999; 99US-0169983.
 PR 09-MAR-2000; 2000US-0188020.
 XX
 XX (CHEO/) CHEO D.
 PA (BRAS/) BRASCH M A.
 PA (TEME/) TEMPLE G F.
 PA (HART/) HARTLEY J L.
 PA (BYRD/) BYRD D R N.
 XX
 PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
 XX
 XX WPI; 2001-356174/37.
 DR
 XX
 PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one
 PT or more recombination sites in the presence of recombination proteins,
 PT e.g. Cre -
 XX
 XX Disclosure; Fig 24A; 357pp; English.
 PS
 XX
 CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination
 CC site nucleic acid sequences, and PCR primers of the invention. The
 CC att sequences are recognised by the recombination protein lambda
 CC integrase (Int). The invention is a new method of producing a population
 CC of hybrid nucleic acids comprising mixing at least a first population of
 CC nucleic acids comprising one or more recombination sites with at least
 CC one target nucleic acid comprising one or more recombination sites and
 CC causing some or all of the nucleic acids to recombine with all or some of
 CC the target nucleic acids. The method is useful for producing a population
 CC of hybrid nucleic acids which may be the same or different. The nucleic
 CC acids may be used to express therapeutic proteins or peptides and they
 CC may also be used to create novel fusion proteins by expressing different
 CC sequences linked to each other. The method allows simultaneous cloning of
 CC two or more different nucleic acids.
 XX
 SQ Sequence 27 BP; 6 A; 4 C; 6 G; 11 T; 0 other;
 Query Match 100.0%; Score 25; DB 22; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||
 RESULT 10
 ABZ58732
 ID ABZ58732 standard; DNA; 27 BP.
 XX
 AC ABZ58732;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE Att site nucleotide sequence attP1.
 XX
 XX Nucleic acid insertion; recombination; nucleic acid selection;
 KW nucleic acid isolation; att; ds.
 XX
 OS Synthetic.
 OS
 XX WO200295055-A2.
 PN
 XX 28-NOV-2002.
 PD
 XX 21-MAY-2002; 2002WO-US15947.
 PF
 XX 21-MAY-2001; 2001US-291973P.
 PR
 XX (INVI-) INVITROGEN CORP.
 PA
 XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
 PI
 XX

PN WO200259294-A1.
XX
XX PD
XX PD
XX PD
XX PF 24-JAN-2002; 2002WO-AU00073.
XX PF 26-JAN-2001; 2001US-364067P.
XX PR 29-NOV-2001; 2001US-333743P.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PA Wesley S, Waterhouse P, Helliwell C;
XX PI WPI; 2002-682669/73.
XX DR
XX PT New vectors comprising operably linked DNA fragments having an origin
XX PT of replication, a selectable marker and a chimeric DNA construct,
XX PT useful for silencing target nucleic acids and for producing large
XX PT amounts of double-stranded RNA -
XX PS
XX PS Claim 12; Page 15; 104pp; English.
XX CC The present invention describes a vector (I) comprising operably linked
XX CC DNA fragments having: (a) origin of replication allowing replication in a
XX CC recipient cell, preferably in bacteria such as *Escherichia coli*;
XX CC (b) selectable marker region capable of being expressed in the recipient
XX CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
XX CC promoter region capable of being recognized by RNA polymerases of a
XX CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
XX CC third and fourth recombination sites; (iii) 3' transcription terminating
XX CC and polyadenylation region functional in the eukaryotic cell. The first
XX CC and fourth recombination sites, or the second and third recombination
XX CC sites are capable of reacting with a same recombination site, and
XX CC preferably are identical. The first and second recombination sites, or
XX CC the third and fourth recombination sites, do not recombine with each
XX CC other or with a same recombination site. The vector is useful for
XX CC producing large amounts of double-stranded RNA which can be used for
XX CC silencing target nucleic acid sequences. The vectors can also be used to
XX CC convert a DNA fragment into an inverted repeat structure. Plants
XX CC transformed with a vector from the present invention can be used in a
XX CC conventional breeding scheme to produce more plants with the same
XX CC characteristics or to introduce a chimeric gene for reduction of the
XX CC phenotypic expression of nucleic acids. The present sequence represents
XX CC the core sequence of recombination site attB1 which is given in the
XX CC exemplification of the present invention.
XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTGACAAAGTTGG 25
RESULT 7
ACCA4664
ID ACCA4664 standard; DNA; 25 BP.
XX AC
XX AC ACCA4664;
XX DT 29-MAY-2003 (first entry)
XX DE
XX DE Recombination site related oligonucleotide SEQ ID NO:55.
XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX KW Platform artificial chromosome expression system; PCR primer; ss.
XX OS
XX OS Synthetic.

PN WO200297059-A2.
XX
XX PD
XX PD
XX PD
XX PF 30-MAY-2002; 2002WO-US17452.
XX PF 30-MAY-2001; 2001US-294758P.
XX PR 21-MAR-2002; 2002US-366891P.
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX PA Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX PI Stewart S, Shellard J;
XX PI WPI; 2003-140461/13.
XX DR
XX DR Novel eukaryotic chromosome comprising one or many att sites which
XX PT permits site-directed integration in the presence of lambda-integrase,
XX PT useful for site-specific recombination-directed integration of DNA of
XX PT interest -
XX PS
XX PS Claim 43; Page 143; 272pp; English.
XX CC The present invention describes a eukaryotic chromosome (I) comprising
XX CC one or several att sites, where an att site is heterologous to the
XX CC chromosome, and permits site-directed integration in the presence of
XX CC lambda-integrase. Also described: (1) a platform artificial chromosome
XX CC expression system (ACes) (II) comprising several sites that participate
XX CC in recombinase catalysed recombination; and (2) a method (M1) for
XX CC introducing a heterologous nucleic acid into a platform artificial
XX CC chromosome. (I) can be used in gene therapy. (M1) is useful for
XX CC introducing a heterologous nucleic acid molecule into a platform
XX CC artificial chromosome, preferably an ACes. (II) is useful for producing a
XX CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
XX CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
XX CC by a carrier system, microinjection, microcell fusion, electroporation,
XX CC microprojectile bombardment or direct DNA transfer into an embryonic
XX CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
XX CC nucleic acid that encodes a therapeutic product which is useful for
XX CC making a library of ACes comprising random portions of a genome. ACC44612
XX CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
XX CC exemplification of the present invention.
XX SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
Query Match 100.0%; Score 25; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTGACAAAGTTGG 25
RESULT 8
ABT16634
ID ABT16634 standard; DNA; 25 BP.
XX AC
XX AC ABT16634;
XX DT 03-APR-2003 (first entry)
XX DT
XX DE Artificial plant chromosome related oligo SEQ ID No 46.
XX KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
XX KW blood factor; herbicide; stress; agronomical; nutrient quality;
XX KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
XX KW ds.
XX OS
XX OS Unidentified.
XX PN WO200296923-A1.

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 4
AAF55749
ID AAF55749 standard; DNA; 25 BP.

XX AAF55749;

AC 12-APR-2001 (first entry)

DT Recombination site attP1.

DE Recombination site; cloning; att; ss.

XX Unidentified.

OS US6171861-B1.

XX 09-JAN-2001.

XX 12-JAN-1998; 98US-0005476.

XX 07-JUN-1996; 96US-0663002.

XX 07-JUN-1995; 95US-0486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 2001-136877/14.

XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host -
XX Claim 25; Column 46; 73pp; English.

XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention.

XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;

QY Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 5

AAC87880

ID AAC87880 standard; DNA; 25 BP.

XX AAC87880;

XX 02-MAR-2001 (first entry)

XX Escherichia coli core region recombinant site attP1 SEQ ID NO:15.

XX Core region; recombination site; cloning; chimeric DNA;
XX characteristic; mutation; att site; lox site; ss.
XX Escherichia coli.

OS US6143557-A.

XX 07-NOV-2000.

XX 20-JAN-1999; 99US-0233493.

XX 07-JUN-1996; 96US-0663002.

XX 12-JAN-1998; 98US-0005476.

XX 07-JUN-1995; 95US-0486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation -

XX Claim 1; Column 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)

XX comprising a first nucleic acid sequence having a defined sequence

XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,

XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described

XX are: (1) an isolated nucleic acid molecule (II) comprising a first

XX mutated recombination site that removes one or more stop codons from the

XX recombination site or avoids hairpin formation, the recombination site

XX being an att or lox site; (2) an isolated nucleic acid molecule (III)

XX comprising a first att recombination site comprising a mutation that

XX enhances recombination specificity; (3) vectors (IV) comprising the

XX above mentioned nucleic acids; and (4) cells comprising the above

XX mentioned nucleic acids or (IV). The nucleic acids are used in

XX engineering a core region of a given recombination site to provide

XX mutative sites suitable for subcloning reactions. The use of nucleic

XX acids for obtaining engineered recombination in vitro or in vivo makes

XX the methods for DNA or RNA subcloning, highly specific, rapid, and

XX less labour intensive.

XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;

QY Query Match 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 6

ABQ82127

ID ABQ82127 standard; DNA; 25 BP.

XX ABQ82127;

XX 11-DEC-2002 (first entry)

XX Core sequence of recombination site attP1 SEQ ID NO:10.

XX Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ss.

OS Synthetic.

```
PT vitro or in vivo
XX
PS Claim 14; Page 56; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA.
XX
SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;

  Query Match      100.0%; Score 25; DB 18; Length 25;
  Best Local Similarity 100.0%; Pred. No. 0.25;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 2
AAX78949
ID AAX78949 standard; DNA; 25 BP.
XX
AC AAX78949;
XX
DT 17-AUG-1999 (first entry)
XX
DE Oligonucleotide #15 for recombination and cloning method.
XX
KW Cloning; donor; recombination site; vector; chimeric; ss.
XX
OS Synthetic.
XX
FN WO921977-A1.
XX
PD 06-MAY-1999.
XX
PF 26-OCT-1998; 98WO-US22589.
XX
PR 23-OCT-1998; 98US-0177387.
XX
PR 24-OCT-1997; 97US-0065930.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Braesch MA, Fox DK, Hartley JL, Temple GP;
XX
DR WPI; 1999-303011/25.
XX
PT New nucleic acid cloning methods
XX
PS Disclosure; Page 162; 185pp; English.
XX
CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one
CC or more desired nucleic acid segments flanked by at least 2
CC recombination sites which do not recombine with each other; (2) one or
CC more vector donor molecules (VDMs) comprising at least 2 recombination
CC sites which do not recombine with each other; and (3) one or more
CC site-specific recombination proteins; (b) incubating the combination to
CC transfer one or more of the desired segments into one or more of the
CC VDMs, thereby producing one or more desired product molecules (PMs). The
CC methods can be used for the efficient and specific recombination of NAM
CC segments. They can be used to generate chimeric DNA or RNA molecules that

  Query Match      100.0%; Score 25; DB 18; Length 25;
  Best Local Similarity 100.0%; Pred. No. 0.25;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 3
AAD14443
ID AAD14443 standard; DNA; 25 BP.
XX
AC AAD14443;
XX
DT 01-NOV-2001 (first entry)
XX
DE Recombination site attP1 DNA.
XX
KW Recombination site; copy number; replicon; recombinatorial cloning;
XX attP1; ds.
XX
OS Unidentified.
XX
FN US6270969-B1.
XX
PD 07-AUG-2001.
XX
PF 20-JAN-1999; 99US-0233492.
XX
PR 07-JUN-1996; 96US-0663002.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2001-488248/53.
XX
PT Methods for apposing nucleic acids comprising an expression signal and
PT a gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under
PT conditions for recombination -
PS Claim 14; Column 18; 76pp; English.
XX
CC The invention relates to a method for apposing an expression signal and
CC a gene or partial gene, using recombinatorial cloning. The method
CC incubates nucleic acids comprising the expression signal and the gene/
CC partial gene in the presence of a recombination protein under conditions
CC sufficient to cause recombination and therefore appose the expression
CC signal and the gene or partial gene. The methods are useful for apposing
CC an expression signal and a gene or partial gene using recombinatorial
CC cloning. The methods are also useful for changing vectors, constructing
CC genes for fusion proteins, changing copy number, changing replicons,
CC cloning into phages, and cloning e.g., PCR products (with an attB site
CC at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
CC The methods are highly specific, rapid, and less labour intensive than
CC prior art methods. The present sequence is a recombination site
CC useful for recombination cloning.
XX
SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;

  Query Match      100.0%; Score 25; DB 22; Length 25;
  Best Local Similarity 100.0%; Pred. No. 0.25;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:05:38 ; Search time 111.5 Seconds
(without alignments)
605.255 Million cell updates/sec

Title: US-10-055-001A-10

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaagtgg 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

```

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	18 AAT48224	attPl core region.
2	25	100.0	25	20 AAX78949	Oligonucleotide #1
3	25	100.0	25	22 AAD14443	Recombination site
4	25	100.0	25	22 AAF55749	Recombination site
5	25	100.0	25	22 AAF55749	Escherichia coli c
6	25	100.0	25	22 ABQ82127	Core sequence of r
7	25	100.0	25	25 ACC44664	Recombination site
8	25	100.0	25	25 ABT16634	Artificial plant c

9	25	100.0	27	22 AAS06179	Phage-lambda recom
10	25	100.0	27	25 ABZ58732	Att site nucleotid
11	25	100.0	233	21 AAC55382	Recombination site
12	25	100.0	4165	21 AAC55524	Donor plasmid pDON
13	25	100.0	4204	21 AAC55522	Donor plasmid pDON
14	25	100.0	4208	21 AAC55523	Donor plasmid pDON
15	25	100.0	4470	21 AAC55521	Donor plasmid pDON
16	25	100.0	4470	21 AAC55521	Destination plasmid
17	25	100.0	4939	21 AAC55525	Donor plasmid pDON
18	25	100.0	5156	21 AAC55526	Donor plasmid pDON
19	25	100.0	5584	21 AAC55532	Donor plasmid pDON
20	25	100.0	5584	25 ABZ58766	Donor plasmid pDON
21	25	100.0	18691	24 ABQ82130	Acceptor vector pA
22	25	100.0	18691	24 ABQ82130	Oligonucleotide #4
23	23.8	95.2	25	20 AAX78977	attP2.P3 core regi
24	23.4	93.6	25	18 AAT48225	Oligonucleotide #1
25	23.4	93.6	25	20 AAX78950	Recombination site
26	23.4	93.6	25	22 AAD14439	Recombination site
27	23.4	93.6	25	22 AAD14444	Recombination site
28	23.4	93.6	25	22 AAF55745	Recombination site
29	23.4	93.6	25	22 AAF55750	Recombination site
30	23.4	93.6	25	22 AAC87876	Escherichia coli c
31	23.4	93.6	25	22 AAC87881	Escherichia coli c
32	23.4	93.6	25	23 AAS14786	Lambda phage int r
33	23.4	93.6	25	24 ABQ82123	Core sequence of r
34	23.4	93.6	25	24 ABQ82128	Core sequence of r
35	23.4	93.6	25	25 ACC44660	Recombination site
36	23.4	93.6	25	25 ACC44665	Recombination site
37	23.4	93.6	25	25 ABT16630	Artificial plant c
38	23.4	93.6	25	25 ABT16635	Artificial plant c
39	23.4	93.6	27	22 AAS06183	Phage-lambda recom
40	23.4	93.6	27	25 ABZ58736	Att site nucleotid
41	23.4	93.6	233	21 AAC55383	Recombination site
42	23.4	93.6	4165	21 AAC55524	Donor plasmid pDON
43	23.4	93.6	4204	21 AAC55522	Donor plasmid pDON
44	23.4	93.6	4208	21 AAC55523	Donor plasmid pDON
45	23.4	93.6	4428	25 ABZ58768	Destination plasmid

ALIGNMENTS

RESULT 1
AAT48224
ID AAT48224 standard; DNA; 25 BP.
XX
AC AAT48224;
XX
DT 20-OCT-1997 (first entry)
XX
DE attPl core region.
XX
KW att recombination site; core region; mutation; enhance; recombination;
XX vector; subcloning; regulation; exchange; ss.
XX Synthetic.
XX
XX WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US10082.
XX
PR 07-JUN-1995; 95US-0486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
DR WPI; 1997-065168/06.
XX
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in

```

PN      JP 1993236997-A/11
PD      17-SEP-1993
PF      28-FEB-1992 JP 1992042829
PI      OKANO KAZUNOBU, KANEARA HIDEKI
PC      C12Q1/68;
CC      strandedness: Single;
CC      topology: Linear.
FEATURES             source
     location/Qualifiers
     1..201
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
BASE COUNT      58 a      27 g      78 t
ORIGIN
Query Match      87.2%; Score 21.8; DB 6; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAAAGTTGG 25
        |||||
        40 GTTCAGCTTTTATACTAAGTTGG 64

Db

RESULT 40
I13139
LOCUS      I13139                201 bp      DNA      linear      PAT 26-JUL-1995
DEFINITION Sequence 18 from patent US 5434049.
ACCESSION I13139
VERSION   I13139.1 GI:910488
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 201)
AUTHORS   Okano,K. and Kambara,H.
TITLE     Separation of polynucleotides using supports having a plurality of
          electrode-containing cells
JOURNAL   Patent: US 5434049-A 18 18-JUL-1995;
FEATURES   Location/Qualifiers
            1..201
             /organism="unknown"
BASE COUNT      58 a      38 c      27 g      78 t
ORIGIN
Query Match      87.2%; Score 21.8; DB 6; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAAAGTTGG 25
        |||||
        40 GTTCAGCTTTTATACTAAGTTGG 64

Db

Search completed: November 6, 2003, 23:06:42
Job time : 602 secs

```

```

ORGANISM      synthetic construct
REFERENCE      artificial sequences.
1
AUTHORS      Goossens,A. and Inz,D.
TITLE        The use of genes encoding membrane transporter pumps to stimulate
              the production of secondary metabolites in biological cells
JOURNAL      Patent: WO 0208388-A 9 24-OCT-2002;
              Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES      Location/Qualifiers
source        1..12789
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
              /note="vector pX7WG2D"
BASE COUNT    3050 a 3326 c 3397 g 3015 t 1 others
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 12789;
Best Local Similarity 95.8%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 3701 GTTCAGCTTTTGTACAAACTTG 3724

RESULT 35
AX356862
LOCUS      AX356862      13274 bp      DNA      linear      PAT 13-FEB-2002
DEFINITION Sequence 20 from Patent WO0206490.
ACCESSION  AX356862
VERSION     AX356862.1 GI:18674110
KEYWORDS    .
SOURCE      synthetic construct
            artificial sequences.
ORGANISM
REFERENCE
AUTHORS      Dudler,R., Schaffrath,U. and Lawton,K.A.
TITLE        Lipoxigenase genes, promoters, transit peptides and proteins
              thereof
JOURNAL      Patent: WO 0206490-A 20 24-JAN-2002;
              Syngenta Participations AG (CH); Universitaet Zuerich (CH)
FEATURES      Location/Qualifiers
source        1..13274
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
BASE COUNT    3343 a 3271 c 3178 g 3482 t
ORIGIN

Query Match      89.6%; Score 22.4; DB 6; Length 13274;
Best Local Similarity 95.8%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 4026 GTTCAGCTTTTGTACAAACTTG 4049

RESULT 36
AF541939/c
LOCUS      AF541939      13990 bp      DNA      linear      SYN 01-DEC-2002
DEFINITION His-3 integration vector pJHAM007, complete sequence.
ACCESSION  AF541939
VERSION     AF541939.1 GI:25988997
KEYWORDS    .
SOURCE      his-3 integration vector pJHAM007
            his-3 integration vector pJHAM007
            artificial sequences; vectors.
ORGANISM
REFERENCE
AUTHORS      Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE        Description of a GATEWAY Destination Vector For High-Throughput
              Construction of Neurospora crassa Histidine-3 (his-3)-Gene

```

```

JOURNAL      Replacement Plasmids
REFERENCE      Unpublished
              2 (bases 1 to 13990)
AUTHORS      Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE        Direct Submission
JOURNAL      Submitted (27-AUG-2002) Biology, Texas A&M University, BSWW #415,
              College Station, TX 77843-3258, USA
FEATURES      Location/Qualifiers
source        1..13990
              /organism="his-3 integration vector pJHAM007"
              /mol_type="genomic DNA"
              /specific_host="Neurospora crassa"
              /db_xref="taxon:211505"
              1..3173
              /note="pGEM13Zf(+)"
              3174..8368
              /note="his-3 left flank; his-3 target integration site"
              8430..8554
              /note="attr1; Gateway; Bacteriophage lambda recombination
              site"
              8804..9463
              /codon_start=1
              /product="chloramphenicol acetyl transferase"
              /protein_id="AAN76304.1"
              /db_xref="GI:25988998"
              /translation="MEKKITGYTTVDISQWHRKEHFEAFQSVAACTYNQTVOLDITAF
              LKTVKKNKHGFYPAFIHILARLMAHSPFRAMKDGELVINDSVHPCTVFEHQETET
              SSLWSEYHDDPQFLHIYSDVACYGENLAYFPKGFIEINMFPVSNPWSTFTSLNV
              ANMDFAPVFTMGKYYTQGDVLMPLAIQVHHAVCDGPHVGMNLNQYCDWEGG
              A"
              9805..10110
              /note="ccdB"
              /codon_start=1
              /product="gyrase target toxin"
              /protein_id="AAN76305.1"
              /db_xref="GI:25988999"
              /translation="MQFKVITYKRSRYKLFVDVQSDIIDTGRRMVIFLAGRLUSD
              KYRELIPVPHIGDESWMRTTDMASVPVSVIGEEVADLSHRENDIKNAIMFWGI"
              10151..10275
              /note="attr2; Gateway; Bacteriophage lambda recombination
              site"
              10419..13990
              /note="his-3 right flank; his-3 target integration site"
BASE COUNT    3385 a 3549 c 3559 g 3497 t
ORIGIN

Query Match      89.6%; Score 22.4; DB 12; Length 13990;
Best Local Similarity 95.8%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 8454 GTTCAGCTTTTGTACAAACTTG 8431

RESULT 37
BD131368
LOCUS      BD131368      25 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
              sites.
ACCESSION  BD131368
VERSION     BD131368.1 GI:23226313
KEYWORDS    JP 2002500861-A/42.
SOURCE      unidentified
            unidentified
            ORGANISM      unclassified.
            1 (bases 1 to 25)
            Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
            Recombinational cloning using nucleic acids having recombination
            Patent: JP 2002500861-A 42 15-JAN-2002;
            LIFE TECHNOLOGIES INC
            OS      Unknown
            PN      JP 2002500861-A/42

```

```

intron      2726..3040
            /note="RpS5"
            /number=3
polyA_signal 3072..3573
            /note="SV40"
            /gene="w"
gene         3574..7697
            /note="mini-white; derived from Drosophila"
            /complement(<7698..8147)
repeat_region /transposon="piggyBac transposable element"
BASE COUNT  2952 a 2528 c 2491 g 3034 t
ORIGIN
1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1030 GTTCAGCTTTTGTACAAACTTG 1007

Query Match      89.6%; Score 22.4; DB 12; Length 11005;
Best Local Similarity 95.8%; Pred. No. 34;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 32
AX196825
LOCUS      AX196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION  AX196825
VERSION    AX196825.1 GI:28565731
KEYWORDS
SOURCE     piggyBac transformation vector pB-UGIR w+
ORGANISM   piggyBac transformation vector pB-UGIR w+
            artificial sequences; vectors.
REFERENCE  1 (bases 1 to 12677)
AUTHORS   Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE     A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 12677)
AUTHORS   Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE     Direct Submission
JOURNAL    Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES             Location/Qualifiers
     source           1..12677
                     /organism="piggyBac transformation vector pB-UGIR w+"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:221642"
     repeat_region    complement(11..>620)
     TATA_signal      632..998
                     /transposon="piggyBac transposable element"
     misc_feature     1003..2713
                     /note="5x UAS hsp70 TATA signal"
     intron           2726..3040
                     /note="RpS5"
                     /number=3
     misc_feature     complement(3076..4788)
                     /note="Gateway recombination cassette A; attR1 CmR ccdB
                     attR2"
     repeat_region    4789..5246
                     /note="SV40"
     gene             5247..9369
                     /gene="w"
     repeat_region    /note="mini-white; derived from Drosophila"
                     /complement(<9370..9819)
                     /transposon="piggyBac transposable element"
BASE COUNT  3423 a 2924 c 2833 g 3497 t
ORIGIN
1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1030 GTTCAGCTTTTGTACAAACTTG 1007

Query Match      89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 34
AX590202
LOCUS      AX590202 12789 bp DNA linear
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION  AX590202
VERSION    AX590202.1 GI:27901286
KEYWORDS   synthetic construct
SOURCE

```

```

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 4760 GTTCAGCTTTTGTACAAACTTG 4783

RESULT 33
AX196825/c
LOCUS      AX196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION  AX196825
VERSION    AX196825.1 GI:28565731
KEYWORDS
SOURCE     piggyBac transformation vector pB-UGIR w+
ORGANISM   piggyBac transformation vector pB-UGIR w+
            artificial sequences; vectors.
REFERENCE  1 (bases 1 to 12677)
AUTHORS   Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE     A toolkit for transformation and mutagenesis in Drosophila using
            piggyBac
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 12677)
AUTHORS   Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE     Direct Submission
JOURNAL    Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
            Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
            27709, USA
FEATURES             Location/Qualifiers
     source           1..12677
                     /organism="piggyBac transformation vector pB-UGIR w+"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:221642"
     repeat_region    complement(11..>620)
     TATA_signal      632..998
                     /transposon="piggyBac transposable element"
     misc_feature     1003..2713
                     /note="5x UAS hsp70 TATA signal"
     intron           2726..3040
                     /note="RpS5"
                     /number=3
     misc_feature     complement(3076..4788)
                     /note="Gateway recombination cassette B; attR1 CmR ccdB
                     attR2"
     polyA_signal     4789..5246
                     /note="SV40"
     gene             5247..9369
                     /gene="w"
     repeat_region    /note="mini-white; derived from Drosophila"
                     /complement(<9370..9819)
                     /transposon="piggyBac transposable element"
BASE COUNT  3423 a 2924 c 2833 g 3497 t
ORIGIN
1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1030 GTTCAGCTTTTGTACAAACTTG 1007

Query Match      89.6%; Score 22.4; DB 12; Length 12677;
Best Local Similarity 95.8%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 1030 GTTCAGCTTTTGTACAAACTTG 1007

RESULT 34
AX590202
LOCUS      AX590202 12789 bp DNA linear
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION  AX590202
VERSION    AX590202.1 GI:27901286
KEYWORDS   synthetic construct
SOURCE

```

```

/codon_start=1
/product="CcdB"
/protein_id="AAM62301.1"
/db_xref="GI:21552738"
/translation="MOKKVTYKRSRYRLFDVQSDIIDTPGRMVIPASARLLSD
KVSRELYPVVHIGDESRWMTTDMASVPVSVIGEEVADLUSHRENDIKNAINLFWGI"
1610..1736
misc_feature
/notes="attr2 of Gateway conversion cassette frame A"
1762..2048
misc_feature
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
repeat_region
/notes="antisense orientation of Gateway conversion
cassette frame A containing attr1-R2 repeats, Cmr gene and
ccdB gene"
misc_feature
complement(2073..2199)
/notes="attr2 of Gateway conversion cassette frame A"
gene
complement(2241..2546)
/genes="ccdB"
CDS
complement(2241..2546)
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62303.1"
/db_xref="GI:21552740"
/translation="MOKKVTYKRSRYRLFDVQSDIIDTPGRMVIPASARLLSD
KVSRELYPVVHIGDESRWMTTDMASVPVSVIGEEVADLUSHRENDIKNAINLFWGI"
complement(2888..3547)
gene
/genes="Cmr"
complement(2888..3547)
CDS
/genes="Cmr"
/functions="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62302.1"
/db_xref="GI:21552739"
/translation="MEKKTGYTTVDISQWKRHEPFAQSVQCTVNOTVQIDITAF
LKTWKHKHFYPAFHLARLANNHPEPFAKMGDELVWDSVHPCYTVFHEQTFF
SSLWSEYHDDFRLHIYQSDVACYGELAYFFPKFIENFFVSNAPWVSFTSEDLNV
ANMNFPAFPTVTKYITQGDVKVLMPLAIQVHRAVCDGPHVGRVNELOQYCDWQGG
A"
misc_feature
complement(3657..3783)
/notes="attr1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 9019;
Best Local Similarity 95.8%; Pred. No. 35;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
Db 53 GTTCAGCTTTTGTACAACTTG 30

RESULT 30
AY196824 LOCUS 11005 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGateway w+
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS piggyBac transformation vector pB-UGateway w+
ORGANISM artificial sequences; vectors.
REFERENCE
1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
source
1..11005
/organisms="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..2620)
repeat_region
/transposon="piggyBac transposable element"
643..999
TATA_signal
1003..2713
/notes="5x UAS hsp70 TATA signal"
misc_feature
1003..2713
/notes="Gateway recombination cassette A; attr1 Cmr ccdB
attr2"

```

```

REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
Location/Qualifiers
1..11005
/organisms="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..2620)
repeat_region
/transposon="piggyBac transposable element"
643..999
TATA_signal
1003..2713
/notes="5x UAS hsp70 TATA signal"
misc_feature
1003..2713
/notes="Gateway recombination cassette A; attr1 Cmr ccdB
attr2"
2726..3040
intron
/notes="RpS5"
/number=3
polyA_signal
3072..3573
/notes="SV40"
gene
3574..7697
/genes="w"
/notes="mini-white; derived from Drosophila"
complement(<7698..8147)
repeat_region
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 11005;
Best Local Similarity 95.8%; Pred. No. 34;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTG 24
|||||
Db 3089 GTTCAGCTTTTGTACAACTTG 3112

RESULT 31
AY196824/c LOCUS 11005 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS piggyBac transformation vector pB-UGateway w+
SOURCE piggyBac transformation vector pB-UGateway w+
ORGANISM artificial sequences; vectors.
REFERENCE
1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA
FEATURES
source
1..11005
/organisms="piggyBac transformation vector pB-UGateway w+"
/mol_type="genomic DNA"
/db_xref="taxon:221641"
complement(11..2620)
repeat_region
/transposon="piggyBac transposable element"
643..999
TATA_signal
1003..2713
/notes="5x UAS hsp70 TATA signal"
misc_feature
1003..2713
/notes="Gateway recombination cassette A; attr1 Cmr ccdB
attr2"

```



```

repeat_region
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26..1733
/notes="sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, Cmr gene and ccdB
gene"
misc_feature
26..152
/notes="attR1 of Gateway conversion cassette frame A"
262..921
/genes="Cmr"
262..921
/genes="Cmr"
262..921
/genes="Cmr"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62300.1"
/db_xref="GI:21552737"
/translation="MEKKITGYTTVDISQWHRKEHFEAFQSVACQTYNQTVDITAF
LKTVKKNKHFFYPAFIIHLARLMAHPEFRMAKDGELVIWDSVHPCYTVFHEQTET
SSLWSEYHDDRFQFLHYISQDVACYGENLAVFPKGFIEFMFVSANPWVSTFDLNV
ANMNDFFAPVFTMGKYVTQGDVKVLMPLAIQVHHAFCDCGFHVGRLNELQQYCDQWQGG
A"
1263..1568
/genes="ccdB"
1263..1568
/genes="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62301.1"
/db_xref="GI:21552738"
/translation="MQFKVYTYKRSRYELFVDVQSDIIDTPGRMWIPLASARLLSD
KVSRLYPVHHIGDSRWMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
1610..1736
/notes="attR2 of Gateway conversion cassette frame A"
1762..2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
/notes="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, Cmr gene and
ccdB gene"
complement(2073..2199)
/notes="attR2 of Gateway conversion cassette frame A"
complement(2241..2546)
/genes="ccdB"
complement(2241..2546)
/genes="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62303.1"
/db_xref="GI:21552740"
/translation="MQFKVYTYKRSRYELFVDVQSDIIDTPGRMWIPLASARLLSD
KVSRLYPVHHIGDSRWMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
complement(2888..3547)
/genes="Cmr"
complement(2888..3547)
/genes="Cmr"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62302.1"
/db_xref="GI:21552739"
/translation="MEKKITGYTTVDISQWHRKEHFEAFQSVACQTYNQTVDITAF
LKTVKKNKHFFYPAFIIHLARLMAHPEFRMAKDGELVIWDSVHPCYTVFHEQTET
SSLWSEYHDDRFQFLHYISQDVACYGENLAVFPKGFIEFMFVSANPWVSTFDLNV
ANMNDFFAPVFTMGKYVTQGDVKVLMPLAIQVHHAFCDCGFHVGRLNELQQYCDQWQGG
A"

```

```

misc_feature complement(3657..3783)
/notes="attR1 of Gateway conversion cassette frame A"
BASE COUNT 2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match 89.6%; Score 22.4; DB 12; Length 9019;
Best Local Similarity 95.8%; Pred.No. 35;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 3756 GTTCAGCTTTTGTACAAACTTG 3779
|||||

RESULT 29
AF408413/c 9019 bp DNA circular SYN 25-JUN-2002
LOCUS AF408413
DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION AF408413
VERSION AF408413.1 GI:21552736
KEYWORDS
SOURCE Binary vector pJawohl8-RNAi
ORGANISM Binary vector pJawohl8-RNAi
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9019)
AUTHORS Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE Direct Submision
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f.Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
source
1..9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:188084"
/focus
/notes="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803..9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26..1733
/notes="sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, Cmr gene and ccdB
gene"
misc_feature 26..152
/notes="attR1 of Gateway conversion cassette frame A"
262..921
/genes="Cmr"
262..921
/genes="Cmr"
/genes="Cmr"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="Cmr"
/protein_id="AAM62300.1"
/db_xref="GI:21552737"
1263..1568
/genes="ccdB"
1263..1568
/genes="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"

```

```

DEFINITION      Transfection vector pBtdest.
ACCESSION       AJ551314
VERSION         AJ551314.1 GI:29335742
KEYWORDS        amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
                acetyl transferase; control of cell death B protein.
SOURCE          Transfection vector pBtdest
ORGANISM        artificial sequences; vectors.
REFERENCE       1
AUTHORS         Jakoby M.J., Heim, M.A. and Weisshaar, B.
TITLE           Use of a gateway compatible vector for transient plant transfection
JOURNAL         Unpublished
REFERENCE       2 (bases 1 to 4462)
AUTHORS         Jakoby M.J.
TITLE           Direct Submission
JOURNAL         Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
                Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
FEATURES        Location/Qualifiers
                 1..4462
                 /organism="Transfection vector pBtdest"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:225975"
                 31..443
                 /note="35S"
                 421..424
                 /note="35S"
                 456..580
                 /note="attR1"
                 689..1348
                 /gene="cat"
                 689..1348
                 /gene="cat"
                 /codon_start=1
                 /product="chloramphenicol acetyl transferase"
                 /protein_id="CAD83080.1"
                 /db_xref="GI:29335743"
                 /translation="MEKKITGYTVDISQWKRKEHFEAFQSAQCYNTQVLDITAF
                 LKTVKKNKHKFPAPFTHILARLNMHPEFRMAMKDELVIDSVHPCYTVFHEQRTF
                 SLWSYHDDRFQFLHYSDVACYGENLAYPPKGIENMFVSNPWTFSFTDLNV
                 ANMNDFFAPVFMKGYYTQGDVKVLMPLAQVHHAVCBGFHVGRLMNLQOYCDEWQGG
                 A"
                 1690..1995
                 /gene="ccdB"
                 1690..1995
                 /gene="ccdB"
                 /codon_start=1
                 /product="control of cell death B protein"
                 /protein_id="CAD83081.1"
                 /db_xref="GI:29335744"
                 /translations="MQFKVYTYKRESRYRLFVDVQSDIIDTPGRMVPIPLASARLLSD
                 KVSRELYPVVHIGDESWMRTDMSVPVSVIGEVADLSHRENDIKNAINLFWGI"
                 2036..2160
                 /note="attR2"
                 2168..2463
                 /gene="nosR"
                 2168..2463
                 /gene="nosR"
                 2606..3466
                 /gene="amp"
                 2606..3466
                 /gene="amp"
                 /codon_start=1
                 /product="beta lactamase"
                 /protein_id="CAD83082.1"
                 /db_xref="GI:29335745"
                 /translation="MSIQHFRAVALIPFAAFCLVPFAHPETLVKVKDAEDQLGARVGY
                 IELDNGKILDESFRPEFRPMWSTFKVLCGAVLSIRADAGQOLGRRIHYSQNDLVE
                 YSPYVKHTIDGMYIRELCASAITMSDNTAAILLTIGGPKELTAFIHNMGDVRRL
                 DRWPELNEAIPINDERDTTPVAMATTIRKLITGLLTLASRQQLIDWMEADKVGAGPL
                 LRSALPAGWFTADSKGAGERSGIIAALGPDGKPSRIWVIYITGSGATWDERNRQIA
                 EIGASLIKHW"
BASE COUNT     1223 a 995 c 1065 g 1179 t
ORIGIN

```

```

Query Match      89.6%; Score 22.4; DB 12; Length 4462;
Best Local Similarity 95.8%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 480 GTTCAGCTTTTGTACAAACTTG 457

RESULT 27
AX306327/c
LOCUS           AX306327 5148 bp DNA linear PAT 11-DEC-2001
DEFINITION      Sequence 10 from Patent WO0188121.
ACCESSION       AX306327
VERSION         AX306327.1 GI:17645566
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1
AUTHORS         Plaetinck, G., Renard, J.P. and Sogaert, T.
TITLE           Vector constructs
JOURNAL         Patent: WO 0188121-A 10 22-NOV-2001;
                Devgen NV (BE)
FEATURES        Location/Qualifiers
                 1..5148
                 /organism="synthetic construct"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:32630"
                 /note="Plasmid pGN39"
BASE COUNT     1359 a 1199 c 1279 g 1311 t
ORIGIN

Query Match      89.6%; Score 22.4; DB 6; Length 5148;
Best Local Similarity 95.8%; Pred. No. 39;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
|||||
Db 171 GTTCAGCTTTTGTACAAACTTG 148

RESULT 28
AF408413
LOCUS           AF408413 9019 bp DNA circular SYN 25-JUN-2002
DEFINITION      Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION       AF408413
VERSION         AF408413.1 GI:21552736
KEYWORDS        Binary vector pJawohl8-RNAi
SOURCE          Binary vector pJawohl8-RNAi
ORGANISM        artificial sequences; vectors.
REFERENCE       1 (bases 1 to 9019)
AUTHORS         Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
TITLE           pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL         Unpublished
REFERENCE       2 (bases 1 to 9019)
AUTHORS         Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
TITLE           Direct Submission
JOURNAL         Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
                f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
                Germany
FEATURES        Location/Qualifiers
                 1..9019
                 /organism="Binary vector pJawohl8-RNAi"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:188084"
                 /focus
                 /note="binary plant gene silencing vector for one-step
                 cloning of inverted sequences"
                 3803..9019
                 /organism="Binary vector pJawohl8-RNAi"
BASE COUNT     3803 a 9019
ORIGIN

```

Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 24
AX684690/c
LOCUS
DEFINITION
Sequence 9 from Patent WO224865.
ACCESSION
AX684690
VERSION
AX684690.1 GI:29371240
KEYWORDS
SOURCE
ORGANISM
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

REFERENCE
1
Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
Modulation of secondary metabolite production by zinc binuclear
cluster proteins
Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
LOCATION/Qualifiers
1. .35
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"

BASE COUNT 14 a 7 c 7 g 7 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 35;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 35 GTTCAGCTTTTGTACAAACTTG 12

RESULT 25
AX703501/c
LOCUS
DEFINITION
Sequence 63 from Patent WO206653.
ACCESSION
AX703501
VERSION
AX703501.1 GI:29538461
KEYWORDS
SOURCE
ORGANISM
Synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1
Li,M. and Liu,Y.C.
Procarvetic libraries and uses
Patent: WO 0206653-A 63 29-AUG-2002;
Xencor (US)
LOCATION/Qualifiers
1. .1846
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 527 a 381 c 434 g 504 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 1846;
Best Local Similarity 95.8%; Pred. No. 48;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 25 GTTCAGCTTTTGTACAAACTTG 2

RESULT 26
VFO551314/c
LOCUS
VFO551314
4462 bp
DNA
circular SYN 27-MAR-2003

AX498619 25 bp DNA linear PAT 26-SEP-2002
Sequence 9 from Patent EP1229113.
ACCESSION
AX498619
VERSION
AX498619.1 GI:23343416
KEYWORDS
SOURCE
ORGANISM
unidentified
unidentified
unclassified.

REFERENCE
1
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: EP 1229113-A 9 07-AUG-2002;
INVITROGEN CORPORATION (US)
LOCATION/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24
Db 1 GTTCAGCTTTTGTACAAACTTG 24

RESULT 23
BD131335
LOCUS
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION
BD131335
VERSION
BD131335.1 GI:23226280
KEYWORDS
JP 2002500861-A/9.
SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
1 (bases 1 to 25)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational cloning using nucleic acids having recombination
sites.
Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
OS
Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1. .25
/organism="Unknown".
FT Location/Qualifiers
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTG 24

```
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 18
BD131342      25 bp      DNA      linear      PAT 18-SEP-2002
LOCUS
DEFINITION      Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION      BD131342
VERSION      BD131342.1 GI:23226287
KEYWORDS      JF 2002500861-A/16.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE      Recombinational cloning using nucleic acids having recombination
JOURNAL      Patent: JP 2002500861-A 16 15-JAN-2002;
FEATURES      LIFE TECHNOLOGIES INC
COMMENT      OS      Unknown
PN      JP 2002500861-A/16
PD      15-JAN-2002
PF      26-OCT-1998 JP 2000518069
PR      24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC      Description of Unknown Organism: recombination products FH
Key source      1. .25
Location/Qualifiers
FT source      1. .25
/organism="Unknown".
FEATURES      source
               Location/Qualifiers
               1. .25
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 19
AR124529      25 bp      DNA      linear      PAT 16-MAY-2001
LOCUS
DEFINITION      Sequence 9 from patent US 6171861.
ACCESSION      AR124529
VERSION      AR124529.1 GI:14109890
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: US 6171861-A 9 09-JAN-2001;
FEATURES      Location/Qualifiers
               1. .25
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match      93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 20
AR163180      25 bp      DNA      linear      PAT 17-OCT-2001
LOCUS
DEFINITION      Sequence 9 from patent US 6270969.
ACCESSION      AR163180
VERSION      AR163180.1 GI:16233689
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: US 6270969-A 9 07-AUG-2001;
FEATURES      Location/Qualifiers
               1. .25
               /organism="unknown"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 21
AX491648      25 bp      DNA      linear      PAT 16-AUG-2002
LOCUS
DEFINITION      Sequence 9 from Patent EP1227147.
ACCESSION      AX491648
VERSION      AX491648.1 GI:22324156
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1227147-A 9 31-JUL-2002;
FEATURES      Location/Qualifiers
               1. .25
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 22
AX491648      25 bp      DNA      linear      PAT 16-AUG-2002
LOCUS
DEFINITION      Sequence 9 from Patent EP1227147.
ACCESSION      AX491648
VERSION      AX491648.1 GI:22324156
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1227147-A 9 31-JUL-2002;
FEATURES      Location/Qualifiers
               1. .25
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24
```

```
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 20
AR163180      25 bp      DNA      linear      PAT 17-OCT-2001
LOCUS
DEFINITION      Sequence 9 from patent US 6270969.
ACCESSION      AR163180
VERSION      AR163180.1 GI:16233689
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: US 6270969-A 9 07-AUG-2001;
FEATURES      Location/Qualifiers
               1. .25
               /organism="unknown"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 21
AX491648      25 bp      DNA      linear      PAT 16-AUG-2002
LOCUS
DEFINITION      Sequence 9 from Patent EP1227147.
ACCESSION      AX491648
VERSION      AX491648.1 GI:22324156
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1227147-A 9 31-JUL-2002;
FEATURES      Location/Qualifiers
               1. .25
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24

RESULT 22
AX491648      25 bp      DNA      linear      PAT 16-AUG-2002
LOCUS
DEFINITION      Sequence 9 from Patent EP1227147.
ACCESSION      AX491648
VERSION      AX491648.1 GI:22324156
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1
AUTHORS      Hartley,J.L. and Brasch,M.A.
TITLE      Recombinational cloning using engineered recombination sites
JOURNAL      Patent: EP 1227147-A 9 31-JUL-2002;
FEATURES      Location/Qualifiers
               1. .25
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      4 g      12 t
ORIGIN
Query Match      89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTG 24
   |||||
Db 1 GTTCAGCTTTTGTACAAAGTTG 24
```

```

DEFINITION      Sequence 8 from Patent WO0174861.
ACCESSION       AX269137
VERSION         AX269137.1  GI:16542057
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.

REFERENCE       1
AUTHORS         Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
TITLE           Compositions and methods for tissue specific gene regulation
                therapy
JOURNAL         MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES        Location/Qualifiers
                1..25
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                /note="Synthetically generated vector sequence"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match    93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches        24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
    |||||||
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 14
AX491650
LOCUS           AX491650 25 bp DNA linear PAT 16-AUG-2002
DEFINITION      Sequence 11 from Patent EP1227147.
ACCESSION       AX491650
VERSION         AX491650.1  GI:22324158
KEYWORDS        unidentified
SOURCE          unidentified
ORGANISM        unclassified.

REFERENCE       1
AUTHORS         Hartley,J.L. and Brasch,M.A.
TITLE           Recombinational cloning using engineered recombination sites
JOURNAL         INVITROGEN CORPORATION (US)
FEATURES        Location/Qualifiers
                1..25
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match    93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches        24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
    |||||||
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 15
AX491655
LOCUS           AX491655 25 bp DNA linear PAT 16-AUG-2002
DEFINITION      Sequence 16 from Patent EP1227147.
ACCESSION       AX491655
VERSION         AX491655.1  GI:22324163
KEYWORDS        unidentified
SOURCE          unidentified
ORGANISM        unclassified.

REFERENCE       1
AUTHORS         Hartley,J.L. and Brasch,M.A.
TITLE           Recombinational cloning using engineered recombination sites
JOURNAL         INVITROGEN CORPORATION (US)
FEATURES        Location/Qualifiers
                1..25
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match    93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches        24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
    |||||||
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 16
AX498621
LOCUS           AX498621 25 bp DNA linear PAT 26-SEP-2002
DEFINITION      Sequence 11 from Patent EP1229113.
ACCESSION       AX498621
VERSION         AX498621.1  GI:23343418
KEYWORDS        unidentified
SOURCE          unidentified
ORGANISM        unclassified.

REFERENCE       1
AUTHORS         Hartley,J.L. and Brasch,M.A.
TITLE           Recombinational cloning using engineered recombination sites
JOURNAL         INVITROGEN CORPORATION (US)
FEATURES        Location/Qualifiers
                1..25
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match    93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches        24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
    |||||||
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25

RESULT 17
AX498626
LOCUS           AX498626 25 bp DNA linear PAT 26-SEP-2002
DEFINITION      Sequence 16 from Patent EP1229113.
ACCESSION       AX498626
VERSION         AX498626.1  GI:23343423
KEYWORDS        unidentified
SOURCE          unidentified
ORGANISM        unclassified.

REFERENCE       1
AUTHORS         Hartley,J.L. and Brasch,M.A.
TITLE           Recombinational cloning using engineered recombination sites
JOURNAL         INVITROGEN CORPORATION (US)
FEATURES        Location/Qualifiers
                1..25
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN
Query Match    93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches        24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAAGTTGG 25
    |||||||
Db 1 GTTCAGCTTCTTGACAAAGTTGG 25
```

```
PN JP 2002500861-A/43
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1. .25
  /organism='unknown'.
FEATURES
  source
    Location/Qualifiers
      1. .25
        /organism='unidentified'
        /mol_type='genomic DNA'
        /db_xref='taxon:32644'
BASE COUNT 4 a 3 c 5 g 10 t 3 others
ORIGIN
Query Match 95.2%; Score 23.8; DB 6; Length 25;
Best Local Similarity 88.0%; Pred. No. 29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||

RESULT 9
AR124531 25 bp DNA PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 11 from patent US 6171861.
ACCESSION AR124531
VERSION AR124531.1 GI:14109892
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
FEATURES Location/Qualifiers
  source 1. .25
    /organism='unknown'
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||

RESULT 10
AR124536 25 bp DNA PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 16 from patent US 6171861.
ACCESSION AR124536
VERSION AR124536.1 GI:14109897
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 16 09-JAN-2001;
FEATURES Location/Qualifiers
  source 1. .25
    /organism='unknown'
```

```
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||

RESULT 11
AR163182 25 bp DNA PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 11 from patent US 6270969.
ACCESSION AR163182
VERSION AR163182.1 GI:16233692
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 11 07-AUG-2001;
FEATURES Location/Qualifiers
  source 1. .25
    /organism='unknown'
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||

RESULT 12
AR163187 25 bp DNA PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 16 from patent US 6270969.
ACCESSION AR163187
VERSION AR163187.1 GI:16233699
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 16 07-AUG-2001;
FEATURES Location/Qualifiers
  source 1. .25
    /organism='unknown'
BASE COUNT 5 a 4 c 6 g 10 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 43;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
  |||||

RESULT 13
AX269137 25 bp DNA PAT 29-OCT-2001
LOCUS
```

Fri Nov 7 08:08:36 2003

kanamycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; speC gene; spectinomycin resistance protein; transposon Tn7.

SOURCE ORGANISM

Cloning vector pHELLSGATE

artificial sequences; vectors.

REFERENCE

1 Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, O., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.

Construct design for efficient, effective and high-throughput gene silencing in plants

Plant J. 27 (6), 581-590 (2001)

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 18691)

Waterhouse, P.M.

Direct Submission

Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

FEATURES

source

1..18691

/organism="Cloning vector pHELLSGATE"

/mol_type="genomic DNA"

/db_xref="taxon:167049"

/lab_host="Escherichia coli"

/focus

/note="pHELLSGATE is a derivative of cloning vector PART27"

source

1..264

/organism="Escherichia coli K12"

/mol_type="genomic DNA"

/strain="K12"

/db_xref="taxon:83333"

265..448

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

source

449..1442

/organism="Escherichia coli"

/mol_type="genomic DNA"

/db_xref="taxon:562"

1443..7792

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

source

7793..9388

/organism="Escherichia coli"

/mol_type="genomic DNA"

/db_xref="taxon:562"

source

9389..11673

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

source

11674..13019

/organism="Cauliflower mosaic virus"

/mol_type="genomic DNA"

/db_xref="taxon:10641"

source

14660..16258

/organism="Flaveria trinervia"

/mol_type="genomic DNA"

/db_xref="taxon:4227"

source

17922..18691

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

promoter

264..447

/function="NOS promoter"

448..1269

/gene="nptII"

448..1269

CDS

/note="neomycin phosphotransferase II (nptII)"

```

/codon_start=1
/transl_table=11
/product="kanamycin resistance protein"
/protein_id="CAC86252.1"
/db_xref="GI:15982219"
/db_xref="REMTREMBL:CAC86252"
/translation="MAITLSATSLPISARIRAGSPAARVERLFGYDWAQOTIGCSDAALVFLSAQRPVLFVKTDLGALNEQDEARLSWLTATGVCAAVLVDVTEAGRDWLLLAEVFPQDILLSHLPAAEKVSIMADARLHLIDPAICFDQAKHRIARTRMEAGLVQDDLEHQCLAPAEFLARLKARMPDGEDLVVTHGACLPININVENGRSGFLDCGRIGVADRYQDIALATRDIAEELGGEWADRFVLVYIGIAAPDSQRIAFYRLDDEFF"
1443..2148
/note="NOS terminator"
2149..2706
/note="left border"
7793..9388
/transposon="Tn7"
8600..9388
/gene="spec"
8600..9388
/gene="spec"
/codon_start=1
/transl_table=11
/product="spectinomycin resistance protein"
/protein_id="CAC86253.1"
/db_xref="GI:15982220"
/db_xref="REMTREMBL:CAC86253"
/translation="MREAVIAEVSTQSEVVGVIETLLEPTLLAVHLYGSANDGLKXPHSDIDLVTVTTRLDLTTTRALINDLLETASGESEILRAVEVTIVVHDDIIPWRYPKRELOFGWQRNDILAGIPEPATIDIDLITKARESHVALVGPAAELFDVPSQDLFEALNETLWNSPPDWAGDERNVLTLSRIWYSATVGTGIAPKDAADWAMERLPAQYQPVLEAQAQYLGQEDRLASRADQLEEFVHYVKGITTKVVGK"
10706..11324
/note="right border"
11674..13019
/function="35S promoter"
14660..16258
/gene="pdk"
14660..16258
/gene="pdk"
/note="pyruvate orthophosphate dikinase (pdk)"
/number=2
17922..18687
/note="octopine esynthase (ocs) terminator"
BASE COUNT 4837 a 4621 c 4607 g 4626 t
ORIGIN
Query Match 100.0%; Score 25; DB 12; Length 18691;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGTAAGAATTGG 25
|||||
Db 13146 GTTCAGCTTTTGTGTAAGAATTGG 13122

RESULT 8
BD131369
LOCUS
DEFINITION Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131369
VERSION BD131369.1 GI:23226314
KEYWORDS JP 2002500861-A/43.
SOURCE unidentified
ORGANISM unclassified.
1 (bases 1 to 25)
REFERENCE
AUTHORS Hartley, J.L., Brach, M.A., Temple, G.F. and Fox, D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 43 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown

```

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||||
 Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 6
 CVE311874 18691 bp DNA circular SYN 09-JUL-2002
 LOCUS Cloning vector pHELLSGATE.
 DEFINITION AJ311874
 ACCESSION
 VERSION AJ311874.1 GI:15982218
 KEYWORDS kanamycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.

SOURCE Cloning vector pHELLSGATE
 ORGANISM Cloning vector pHELLSGATE
 artificial sequences; vectors.

REFERENCE 1
 AUTHORS Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.
 TITLE Construct design for efficient, effective and high-throughput gene silencing in plants
 JOURNAL Plant J. 27 (6), 581-590 (2001)
 MEDLINE 21461301
 PUBMED 11576441

REFERENCE 2 (bases 1 to 18691)
 AUTHORS Waterhouse, P.M.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

FEATURES
 source
 1..18691
 /organism="Cloning vector pHELLSGATE"
 /mol_type="genomic DNA"
 /db_xref="taxon:167049"
 /lab_host="Escherichia coli"
 /focus
 /note="pHELLSGATE is a derivative of cloning vector PART27"
 1..264
 /organism="Escherichia coli K12"
 /mol_type="genomic DNA"
 /strain="K12"
 /db_xref="taxon:83333"
 265..448
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 449..1442
 /organism="Escherichia coli"
 /mol_type="genomic DNA"
 /db_xref="taxon:562"
 1443..7792
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 7793..9388
 /organism="Escherichia coli"
 /mol_type="genomic DNA"
 /db_xref="taxon:562"
 9389..11673
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 11674..13019
 /organism="Cauliflower mosaic virus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10641"
 14660..16258
 /organism="Flaveria trinervia"
 /mol_type="genomic DNA"
 /db_xref="taxon:4227"

17922..18691
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 264..447
 /function="NOS promoter"
 448..1269
 /gene="nptII"
 448..1269
 /gene="nptII"
 /note="neomycin phosphotransferase II (nptII)"
 /codon_start=1
 /transl_table=11
 /product="kanamycin resistance protein"
 /protein_id="CAC86252.1"
 /db_xref="GI:15982219"
 /db_xref="REMBL:CAC86252"
 /translation="MAITLSATSLPISARIRAGSPAAWVERLFGYDWAQQTIGCSDAALVRLSAQGRPVLFVKTIDUSGALNELQDEARLSWLTATGVPCAAVLVDVYTEAGRDWLL LGEVQDLSHSLAPAEKVSIMADAMRLRLDLPATCFDHOAKHRIERARFMEAG LVDQDLDEHQGLAPAEFLKARMPDGEDLVVTHGDACLPLNINVENGRSGFIDC GRLGVADRYDIALATRDIAEELGGWADRFVLVYGLAAPSQRIFAYELLDEFF"
 1443..2148
 /note="NOS terminator"
 2149..2706
 /note="left border"
 7793..9388
 /transposon="Tn7"
 8600..9388
 /gene="spec"
 8600..9388
 /gene="spec"
 /codon_start=1
 /transl_table=11
 /product="spectinomycin resistance protein"
 /protein_id="CAC86253.1"
 /db_xref="GI:15982220"
 /db_xref="REMBL:CAC86253"
 /translation="MREAVIAEVSTQSEVVGVIERHLEPTLLAVHLYGSAVDGGLKP HSDILLVTVRLDTRRALINDLLETSSAFGESEILRAVEITIVHDDIIPWRYP AKRELQGEWQRNDILAGIPEPATIDILAILLTAKREHSVALVGPAAEELFDPVPEQ DLPEALNETLTWNSPDMAGDERNVLTLSRIWYSAVTGKIAPKDVAAAWMERLPA QYQPVLEARQAYLGQEDRLASRADQLEBEFVHVYKGEITKVVK"
 10706..11324
 /note="right border"
 11674..13019
 /function="35S promoter"
 14660..16258
 /gene="pdk"
 14660..16258
 /gene="pdk"
 /note="pyruvate orthophosphate dikinase (pdk)"
 /number=2
 17922..18687
 /note="octopine esynthase (ocs) terminator"
 BASE COUNT 4837 a 4621 c 4607 g 4626 t
 ORIGIN

Query Match 100.0%; Score 25; DB 12; Length 18691;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
 |||||||
 Db 17792 GTTCAGCTTTTGTACAAAGTTGG 17816

RESULT 7
 CVE311874/c 18691 bp DNA circular SYN 09-JUL-2002
 LOCUS Cloning vector pHELLSGATE.
 DEFINITION AJ311874
 ACCESSION AJ311874
 VERSION AJ311874.1 GI:15982218


```
source 1..25
/organism="unknown"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 2
LOCUS AR163186 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 15 from patent US 6270969.
ACCESSION AR163186
VERSION AR163186.1 GI:16233698
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 15 07-AUG-2001;
FEATURES
source
1..25
Location/Qualifiers
/organism="unknown"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 3
LOCUS AX491654 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 15 from Patent EP1227147.
ACCESSION AX491654
VERSION AX491654.1 GI:22324162
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 15 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 4
LOCUS AX498625 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 15 from Patent EP1229113.
ACCESSION AX498625
VERSION AX498625.1 GI:23343422
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 5
LOCUS BD131341 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131341
VERSION BD131341.1 GI:23226286
KEYWORDS JP 2002500861-A/15.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 15 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT
OS Unknown
PN JP 2002500861-A/15
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products PH
KEY
FT source 1..25
Location/Qualifiers
/organism="Unknown".
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 3 c 6 g 11 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||
Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-10

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaagtgg 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 288711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_ov.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_sy.*

14: gb_vi.*

15: gb_vi.*

16: em_fun.*

17: em_fun.*

18: em_in.*

19: em_mu.*

20: em_mu.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_un.*

30: em_vt.*

31: em_htg_hum.*

32: em_htg_inv.*

33: em_htg_inv.*

34: em_htg_mus.*

35: em_htg_pln.*

36: em_htg_rod.*

37: em_htg_man.*

38: em_htg_vrt.*

39: em_htg_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	25	100.0	25	6	AR124535 Sequence
2	25	100.0	25	6	AR163186 Sequence
3	25	100.0	25	6	AX491654 Sequence
4	25	100.0	25	6	AX498625 Sequence
5	25	100.0	25	6	BD131341 Recombina
6	25	100.0	18691	12	CVB311874
7	25	100.0	18691	12	CVB311874
8	23.8	95.2	25	6	BD131369 Sequence
9	23.4	93.6	25	6	AR124531 Sequence
10	23.4	93.6	25	6	AR124536 Sequence
11	23.4	93.6	25	6	AR163182 Sequence
12	23.4	93.6	25	6	AR163187 Sequence
13	23.4	93.6	25	6	AX269137 Sequence
14	23.4	93.6	25	6	AX491650 Sequence
15	23.4	93.6	25	6	AX491655 Sequence
16	23.4	93.6	25	6	AX498621 Sequence
17	23.4	93.6	25	6	AX498626 Sequence
18	23.4	93.6	25	6	BD131342 Recombina
19	22.4	89.6	25	6	AR124529 Sequence
20	22.4	89.6	25	6	AR163180 Sequence
21	22.4	89.6	25	6	AX491648 Sequence
22	22.4	89.6	25	6	AX498619 Sequence
23	22.4	89.6	25	6	BD131335 Recombina
24	22.4	89.6	35	6	AX684690 Sequence
25	22.4	89.6	1846	6	AX703501 Sequence
26	22.4	89.6	4462	12	VFO551314
27	22.4	89.6	5148	6	AX306327 Sequence
28	22.4	89.6	9019	12	AF08413 Binary ve
29	22.4	89.6	9019	12	AF08413 Binary ve
30	22.4	89.6	11005	12	AY196824 PiggyBac
31	22.4	89.6	11005	12	AY196824 PiggyBac
32	22.4	89.6	12677	12	AY196825 PiggyBac
33	22.4	89.6	12677	12	AY196825 PiggyBac
34	22.4	89.6	12789	6	AX590202 Sequence
35	22.4	89.6	13274	6	AX356862 Sequence
36	22.4	89.6	13990	12	AF541939 His-3 int
37	22	88.0	25	6	BD131368 Recombina
38	21.8	87.2	201	6	AR044609 Sequence
39	21.8	87.2	201	6	E05439 Oligonucleo
40	21.8	87.2	201	6	I13139 Sequence 18
41	21.8	87.2	201	6	I36498 Sequence 18
42	21.8	87.2	243	6	AX092113 Sequence
43	21.8	87.2	361	7	LAMINTATT
44	21.8	87.2	610	6	AX101000 Sequence
45	21.8	87.2	1668	9	MACHSS

ALIGNMENTS

RESULT 1						
AR124535						
LOCUS	AR124535	Sequence 15 from patent US 6171861.	25 bp	DNA	linear	PAT 16-MAY-2001
DEFINITION	AR124535					
ACCESSION	AR124535					
VERSION	AR124535.1	GI:14109896				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Hartley, J.L. and Brasch, M.A.					
TITLE	Recombinational cloning using engineered recombination sites					
JOURNAL	Patent: US 6171861-A 15 09-JAN-2001;					
FEATURES	Location/Qualifiers					

FEATURES
source

Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI071Y1A13"
/tissue="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
232 a 290 c 326 g 241 t 112 others
ORIGIN
Query Match 80.0%; Score 20; DB 13; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CAGCTTCTTGTACAAACTTGT 25
|:|||||
Db 30 CMGCTTTTGTACAACTTGT 9
|:|||||

RESULT 40

EX400983/c
LOCUS
DEFINITION BX400983 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK005YD11 5-PRIME, mRNA sequence.
ACCESSION BX400983
VERSION BX400983.1 GI:30626325
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1058.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK005CB06P1&cluster=1058.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DK005CB06QP1.

FEATURES
source

Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK005YD11"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
283 a 315 c 336 g 239 t 28 others
ORIGIN
Query Match 80.0%; Score 20; DB 13; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CAGCTTCTTGTACAAACTTGT 25
|:|||||

Db 39 CMGCTTTTGTACAAACTTGT 18
|:|||||

Search completed: November 7, 2003, 00:20:57
Job time : 1095.75 secs

```
BASE COUNT      279 a 244 c 318 g 244 t 116 others
ORIGIN
Query Match      80.0%; Score 20; DB 9; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTGTACAAACTTGT 25
    ||||| ||||| ||||| ||||| |||||
Db 33 CAGCTTTTGTACAAACTTGW 12

RESULT 37
BX363509/c
LOCUS
DEFINITION
BX363509 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL001YD08 5-PRIME, mRNA sequence.
ACCESSION
BX363509
VERSION
BX363509.1 GI:30376731
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2356.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DL001DB04QPI&cluster=2356.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DL001DB04QPI.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL001YD08"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/clone_lib="RAMOS CELL LINE"
/notes="1st strand cDNA was primed with a NotI-oligo (dtr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      335 a 140 c 217 g 340 t 169 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTGTACAAACTTGT 25
    ||||| ||||| ||||| ||||| |||||
Db 35 CWGCTTTTGTACAAACTTGT 14

RESULT 38
BX382731
LOCUS
DEFINITION
BX382731 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI085YB18 3-PRIME, mRNA sequence.
ACCESSION
BX382731
```

```
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9393.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI085DA09NP1&cluster=9393.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI085DA09NP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI085YB18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dtr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      219 a 297 c 379 g 218 t 88 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTGTACAAACTTGT 25
    ||||| ||||| ||||| ||||| |||||
Db 775 CTGCTTTTGTACAAACTTGT 796

RESULT 39
BX386369/c
LOCUS
DEFINITION
BX386369 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI071YA13 5-PRIME, mRNA sequence.
ACCESSION
BX386369
VERSION
BX386369.1 GI:30436794
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 95.r For more
information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AI0182E07QPI&cluster=95.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AI0182E07QPI.
```



```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 1190)
JOURNAL     Full-length cDNA libraries and normalization
COMMENT     Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9817.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC002AC03QPI&cluster=9817.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC002AC03QPI.

FEATURES             source
1..1190
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC002YE05"
/tissue_type="Neuroblastoma"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      248 a 332 c 362 g 209 t 39 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1190;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CAGCTTCTTGTGACAACTTGT 25
      :|||||
Db      38 CWGCTTTTGTGACAACTTGT 17

RESULT 32
BX463747/c
LOCUS      BX463747      1198 bp      mRNA      linear      EST 22-MAY-2003
DEFINITION BX463747 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION   BX463747
VERSION     BX463747.1 GI:31031557
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 1198)
JOURNAL     Full-length cDNA libraries and normalization
COMMENT     Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3257.f,
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AF001ZF02QPI.

FEATURES             source
1..1198
/mol_type="mRNA"

```

```

/db_xref="taxon:9606"
/clone="CS0DF003YB02"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT      256 a 295 c 337 g 237 t 73 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 1198;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CAGCTTCTTGTGACAACTTGT 25
      :|||||
Db      39 CWGCTTTTGTGACAACTTGT 18

RESULT 33
AL513677/c
LOCUS      AL513677      1201 bp      mRNA      linear      EST 08-MAY-2003
DEFINITION AL513677 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA007ZB09
3-PRIME, mRNA sequence.
ACCESSION   AL513677
VERSION     AL513677.2 GI:30463562
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 1201)
JOURNAL     Full-length cDNA libraries and normalization
COMMENT     Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777171.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BA007ZB09FP1.

FEATURES             source
1..1201
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BA007ZB09"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      212 a 298 c 258 g 272 t 161 others
ORIGIN
Query Match      80.0%; Score 20; DB 9; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CAGCTTCTTGTGACAACTTGT 25
      :|||||
Db      41 CAGCTTTTGTGACAAAGTKGT 20

RESULT 34

```

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3974.f For more information about this cluster, see <http://www.genoscope.cns.fr/>
 cgi-bin/cluster.cgi?seq=CL0BB015ZG02FP1&cluster=3974.f. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CL0BB015ZG02FP1.

FEATURES

source

1. 959
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CL0BB015ZG02"
 /tissue_type="NEUROBLASTOMA"
 /clone_lib="Homo sapiens NEUROBLASTOMA"
 /note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
 Library was not normalized.

BASE COUNT 210 a 203 c 232 g 227 t 87 others

ORIGIN

Query Match 80.0%; Score 20; DB 9; Length 959;
 Best Local Similarity 90.9%; Pred. No. 6.2e+02;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTCACAACTTGT 25

Db 38 CAGCTTCTTGTCACAAAGTGT 17

RESULT 29

AL550767/c

LOCUS 1060 bp mRNA linear EST 31-MAY-2003
 DEFINITION AL550767 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSODI056YC22 5-PRIME, mRNA sequence.

ACCESSION AL550767

VERSION AL550767.2 GI:31272584

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1060)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 15, 2001 this sequence version replaced gi:12888058.

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 629.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>
 cgi-bin/cluster.cgi?seq=CSODI056BB11QPI&cluster=629.f. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI056BB11QPI.

FEATURES

source

1. 1060
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI056YC22"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV

BASE COUNT 243 a 276 c 226 g 257 t 58 others
 ORIGIN sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 80.0%; Score 20; DB 9; Length 1060;
 Best Local Similarity 90.9%; Pred. No. 6.3e+02;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTCACAACTTGT 25

Db 40 CWGCTTTTGTACAACTTGT 19

RESULT 30

BX338865/c

LOCUS 1084 bp mRNA linear EST 02-MAY-2003
 DEFINITION BX338865 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSODI064YH04 5-PRIME, mRNA sequence.

ACCESSION BX338865

VERSION BX338865.1 GI:30335745

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1084)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5957.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>
 cgi-bin/cluster.cgi?seq=CSODI064D020P1&cluster=5957.f. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI064D020P1.

Location/Qualifiers

1. 1084

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI064YH04"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 207 a 276 c 314 g 250 t 37 others

ORIGIN

Query Match 80.0%; Score 20; DB 13; Length 1084;
 Best Local Similarity 90.9%; Pred. No. 6.3e+02;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTCTTGTCACAACTTGT 25

Db 33 CAGCTTTTGTACAACTTGT 12

RESULT 31

BX374761/c

LOCUS 1190 bp mRNA linear EST 08-MAY-2003
 DEFINITION BX374761 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 cDNA clone CSODC002YE05 5-PRIME, mRNA sequence.

ACCESSION BX374761

VERSION BX374761.1 GI:30452336

KEYWORDS EST.

```

source
1. .897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDF027YH18"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT      193 a   211 c   216 g   276 t   1 others
ORIGIN
Query Match      80.0%; Score 20; DB 9; Length 897;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 30 CWGCTTTTCTGTACAAACTTGT 9

RESULT 26
BX395287      910 bp   mRNA   linear   EST 13-MAY-2003
LOCUS
DEFINITION
BX395287      Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CSDD004YF19 5-PRIME, mRNA sequence.
ACCESSION
BX395287
VERSION
BX395287.1 GI:30624532
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 910)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID : CSDD004CC10QF1.
FEATURES
source
Location/Qualifiers
1. .910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDD004YF19"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      238 a   302 c   74 g   233 t   63 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 910;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 825 CAGCTTTCTTGTACAAACTTGT 846

```

```

RESULT 27
BX334648/c
LOCUS
DEFINITION
BX334648      Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI005YI06 5-PRIME, mRNA sequence.
ACCESSION
BX334648
VERSION
BX334648.1 GI:30341342
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 933)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 334.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI005BE03QPI&cluster=334.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI005BE03QF1.
FEATURES
source
Location/Qualifiers
1. .933
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI005YI06"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      254 a   212 c   238 g   227 t   2 others
ORIGIN
Query Match      80.0%; Score 20; DB 13; Length 933;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25
   ||||| ||||| ||||| ||||| |||||
Db 38 CAGCTTTTGTGTACAAACTTGT 17

RESULT 28
AL514767/c
LOCUS
DEFINITION
AL514767      Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB0152G02 3-PRIME, mRNA sequence.
ACCESSION
AL514767
VERSION
AL514767.2 GI:30464652
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 959)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12778260.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

```



```

Query Match      80.8%; Score 20.2; DB 13; Length 991;
Best Local Similarity 88.0%; Pred. No. 5.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 50 GTCTGCTTTTGTGTACAAACTTGT 26

RESULT 23
BX428996/c
LOCUS
DEFINITION
  BX428996 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
  clone CS0DG005YF18 5-PRIME, mRNA sequence.
ACCESSION
  BX428996
VERSION
  EST.
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 7333.f For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0AS009ZC07Q1&cluster=7333.f. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0AS009ZC07Q1.
  Location/Qualifiers
    1..1006
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DG005YF18"
    /tissue_type="B CELLS (RAMOS CELL LINE)"
    /cell_line="RAMOS CELL LINE"
    /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
    with a NotI-oligo(GT) primer. Five prime end enriched,
    double-strand cDNA was digested with NotI and cloned into
    the NotI and EcoRV sites of the pCMVSPORT 6 vector.
    Library was not normalized."
  Library was not normalized."
BASE COUNT      268 a 231 c 306 g 190 t 11 others
ORIGIN
  1..1006
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DG005YF18"
  /tissue_type="B CELLS (RAMOS CELL LINE)"
  /cell_line="RAMOS CELL LINE"
  /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
  with a NotI-oligo(GT) primer. Five prime end enriched,
  double-strand cDNA was digested with NotI and cloned into
  the NotI and EcoRV sites of the pCMVSPORT 6 vector.
  Library was not normalized."
  Library was not normalized."

Query Match      80.8%; Score 20.2; DB 13; Length 1006;
Best Local Similarity 88.0%; Pred. No. 5.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTGTACAAACTTGT 25
Db 42 GTCTGCTTTTGTGTACAAACTTGT 18

RESULT 24
BX333971/c
LOCUS
DEFINITION
  BX333971 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
  cDNA clone CS0DD004YN23 5-PRIME, mRNA sequence.
ACCESSION
  BX333971
VERSION
  EST.
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 1734.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DF027YH18 5-PRIME, mRNA sequence.
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DF027YH18.
  Location/Qualifiers
    1..894
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DD004YN23"
    /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
    /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
    /note="Five prime end enriched, double-strand cDNA was
    digested with NotI and EcoRV sites of the pCMVSPORT 6 vector.
    Library was normalized."
  Library was normalized."
BASE COUNT      148 a 332 c 233 g 173 t 8 others
ORIGIN
  1..894
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DD004YN23"
  /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
  /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
  /note="Five prime end enriched, double-strand cDNA was
  digested with NotI and EcoRV sites of the pCMVSPORT 6 vector.
  Library was normalized."
  Library was normalized."

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 894)
AUTHORS
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
  Full-length cDNA libraries and normalization
JOURNAL
  Unpublished
COMMENT
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 9435.f For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DD004CG12QP1&cluster=9435.f. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DD004CG12QP1.
  Location/Qualifiers
    1..894
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DD004YN23"
    /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
    /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
    /note="Five prime end enriched, double-strand cDNA was
    digested with NotI and EcoRV sites of the pCMVSPORT 6 vector.
    Library was normalized."
  Library was normalized."
BASE COUNT      148 a 332 c 233 g 173 t 8 others
ORIGIN
  1..894
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DD004YN23"
  /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
  /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
  /note="Five prime end enriched, double-strand cDNA was
  digested with NotI and EcoRV sites of the pCMVSPORT 6 vector.
  Library was normalized."
  Library was normalized."

Query Match      80.0%; Score 20; DB 13; Length 894;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTCTGTACAAACTTGT 25
Db 37 CWGCTTTTGTGTACAAACTTGT 16

RESULT 25
AL538354/c
LOCUS
DEFINITION
  AL538354 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
  CS0DF027YH18 5-PRIME, mRNA sequence.
ACCESSION
  AL538354
VERSION
  EST.
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 1734.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DF027YH18 5-PRIME, mRNA sequence.
  http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DF027YH18.
  Location/Qualifiers
    1..894
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DF027YH18 5-PRIME, mRNA sequence."
    /tissue_type="FETAL BRAIN"
    /clone_lib="Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
    CS0DF027YH18 5-PRIME, mRNA sequence."
  Library was not normalized."
  Library was not normalized."
BASE COUNT      268 a 231 c 306 g 190 t 11 others
ORIGIN
  1..894
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DF027YH18 5-PRIME, mRNA sequence."
  /tissue_type="FETAL BRAIN"
  /clone_lib="Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
  CS0DF027YH18 5-PRIME, mRNA sequence."
  Library was not normalized."
  Library was not normalized."

```

```

ACCESSION      BX457051
VERSION        BX457051.1  GI:31034832
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
AUTHORS        1. (bases 1 to 956)
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished
COMMENT        Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 6437.r For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0CAP005DH01Q1P1&cluster=6437.r. Contact :
               Peng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0CAP005DH01Q1P1.
               Location/Qualifiers
                 1..956
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="CS0CAP005YP02"
                   /tissue_type="THYMUS"
                   /clone_lib="Homo sapiens THYMUS"
                   /notes="vector: pCMVSPORT 6; 1st strand cDNA was primed
                   with a NotI-oligo(dT) primer. Five prime end enriched,
                   double-strand cDNA was digested with Not I and cloned into
                   the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                   Library was not normalized."
BASE COUNT     209 a      286 c      234 g      220 t      7 others
ORIGIN
Query Match      80.8%; Score 20.2; DB 13; Length 956;
Best Local Similarity 88.08; Pred.No.5.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GTTCAGCTTTCTGTACAAACTTGT 25
    |||||
Db   40  GCTCTGCTTTTCTGTACAAACTTGT 16

RESULT 21
BX422399/c
LOCUS          BX422399 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION     CS0DM004YD15 5-PRIME, mRNA sequence.
ACCESSION      BX422399
VERSION        BX422399.1  GI:30655319
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
AUTHORS        1. (bases 1 to 973)
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished
COMMENT        Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 7228.f For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DM004CB08QP1&cluster=7228.f. Contact :

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5261647"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 95"
/notes="Organ: brain; Vector: pBluescriptPR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTIVN-3', size-selected for average insert size 2.5 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 259 a 131 c 194 g 233 t
ORIGIN

Query Match 80.8%; Score 20.2; DB 12; Length 817;
Best Local Similarity 88.0%; Pred. No. 4.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 542 GTTCAAATTTCTTGACAAATTTGT 566

RESULT 18
BF669965 884 bp mRNA linear EST 21-DEC-2000
LOCUS 602118471F1 NTH_MGC_56 Homo sapiens cDNA clone IMAGE:4275664 5',
DEFINITION mRNA sequence.
ACCESSION BF669965
VERSION BF669965.1 GI:11943860
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 884)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1094 row: n column: 17
High quality sequence stop: 589.
FEATURES
source
1..884
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4275664"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 56"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggc); SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCAGAGCGGCGCCGACATG-DT(30)BN-3' (where B = A, C, G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 240 a 155 c 247 g 242 t
ORIGIN

Query Match 80.8%; Score 20.2; DB 10; Length 884;
Best Local Similarity 88.0%; Pred. No. 5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 534 GTTAACTTTCTTGACAAATTTGT 558

RESULT 19
AL519260/c 914 bp mRNA linear EST 12-MAY-2003
LOCUS AL519260 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CSODA012XH14 5-PRIME, mRNA sequence.
ACCESSION AL519260
VERSION AL519260.2 GI:30538367
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 914)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12782753.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3874.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODA012DD07QF1&cluster=3874.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID: CSODA012DD07QF1.
FEATURES
source
1..914
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODA012XH14"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.. Library was not normalized."
BASE COUNT 186 a 310 c 254 g 156 t
ORIGIN

Query Match 80.8%; Score 20.2; DB 9; Length 914;
Best Local Similarity 88.0%; Pred. No. 5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTTGACAAACTTGT 25
Db 39 GCTCTGCITTTTGTGACAAACTTGT 15

RESULT 20
BX457051/c 956 bp mRNA linear EST 22-MAY-2003
LOCUS BX457051 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP005YP02
DEFINITION 5-PRIME, mRNA sequence.

```

```

BG573114      706 bp      mRNA      linear      EST 10-APR-2001
LOCUS         602594115F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4721474 5',
DEFINITION    mRNA sequence.
ACCESSION     BG573114
VERSION       BG573114.1 GI:13580767
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 706)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LCM1577 row: n column: 03
              High quality sequence stop: 639.
              Location/Qualifiers
                1..706
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4721474"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NIH_MGC_79"
                /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
                Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc
                ); 5' and 3' adaptors were used in cloning as follows: 5'
                adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
                sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3'
                (where B = A, C, or G and N = A, C, G, or T). Average
                insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
                contained inserts by PCR. This library was enriched for
                full-length clones and was constructed by Clontech
                Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                Library."
              BASE COUNT      205 a      117 c      143 g      241 t
              ORIGIN
                Query Match      80.8%; Score 20.2; DB 10; Length 706;
                Best Local Similarity 88.0%; Pred. No. 4.7e+02;
                Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

              Qy      1 GTTCAGCTTTCTTGTACAAACTTGT 25
                ||| ||||| ||||| ||||| |||||
              Db      186 GTTAAACTTTCTTGTACAAATTTGT 210

              RESULT 16
              BF695849      812 bp      mRNA      linear      EST 22-DEC-2000
              LOCUS         601852207F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076328 5',
              DEFINITION    mRNA sequence.
              ACCESSION     BF695849
              VERSION       BF695849.1 GI:11981257
              KEYWORDS      EST.
              SOURCE        Homo sapiens (human)
              ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              REFERENCE     1 (bases 1 to 812)
              AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
              TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
              JOURNAL       Unpublished

```

```

COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: CLONTECH Laboratories, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LCM929 row: m column: 01
              High quality sequence stop: 637.
              Location/Qualifiers
                1..812
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4076328"
                /tissue_type="primitive neuroectoderm"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NIH_MGC_56"
                /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1:
                SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc);
                Double-stranded cDNA was prepared from cell line RNA. 5'
                and 3' adaptors were used in cloning as follows: 5'
                adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
                sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3'
                (where B = A, C, or G and N = A, C, G, or T). Average
                insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
                contained inserts by PCR. This library was enriched for
                full-length clones and was constructed by Clontech
                Laboratories (Palo Alto, CA)."
              BASE COUNT      259 a      113 c      221 g      219 t
              ORIGIN
                Query Match      80.8%; Score 20.2; DB 10; Length 812;
                Best Local Similarity 88.0%; Pred. No. 4.9e+02;
                Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

              Qy      1 GTTCAGCTTTCTTGTACAAACTTGT 25
                ||| ||||| ||||| ||||| |||||
              Db      535 GTTAAACTTTCTTGTACAAATTTGT 559

              RESULT 17
              BI547007      817 bp      mRNA      linear      EST 05-SEP-2001
              LOCUS         603190229F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5361647 5',
              DEFINITION    mRNA sequence.
              ACCESSION     BI547007
              VERSION       BI547007.1 GI:15434319
              KEYWORDS      EST.
              SOURCE        Homo sapiens (human)
              ORGANISM      Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              REFERENCE     1 (bases 1 to 817)
              AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
              TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
              JOURNAL       Unpublished
              COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
              cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
              Toshiyuki and Piero Carninci (RIKEN)
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LHAM1659 row: i column: 08
              High quality sequence stop: 795.
              Location/Qualifiers
                1..817

```

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6911.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC019BC08QP1&cluster=6911.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC019BC08QP1.

FEATURES

source

1..1145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC019YE16"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 298 a 226 c 244 g 308 t 69 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 1145;
Best Local Similarity 95.5%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTCTTGTCACAACTTGT 25
|||||

Db 39 CAGCTTTTGTGTCACAACTTGT 18
|||||

RESULT 13

BX361644/c

LOCUS 1201 bp mRNA linear EST 05-MAY-2003
DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ001YF12 5-PRIME, mRNA sequence.

ACCESSION BX361644
VERSION BX361644.1 GI:30366552

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7763.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ001DC06QP1&cluster=7763.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ001DC06QP1.

FEATURES

source

1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ001YE12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"

/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 278 a 308 c 341 g 205 t 69 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 1201;
Best Local Similarity 95.5%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCTTTCTTGTCACAACTTGT 25
|||||

Db 35 CAGCTTTTGTGTCACAACTTGT 14
|||||

RESULT 14

B1858895

LOCUS 645 bp mRNA linear EST 10-OCT-2001
DEFINITION 603389227F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5398255 5',
mRNA sequence.

ACCESSION B1858895
VERSION B1858895.1 GI:15999642

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 645)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12015 row: e column: 08
High quality sequence stop: 643.

FEATURES

source

1..645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5398255"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 87"
/note="Organ: Breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 217 a 97 c 158 g 173 t
ORIGIN

Query Match 80.8%; Score 20.2; DB 12; Length 645;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCTTGTCACAACTTGT 25
|||||

Db 524 GTTAAACCTTTCTTGTCACAACTTGT 548
|||||

RESULT 15

FEATURES
source

Location/Qualifiers
1. .934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF014YA08"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT 233 a 233 c 278 g 199 t 1 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 934;
Best Local Similarity 95.5%; Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAACTTGT 25
|||||
Db 35 CAGCTTTTGTACAACTTGT 14

RESULT 10
BX359829/c
LOCUS
DEFINITION BX359829 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI062YG23 5-PRIME, mRNA sequence.
ACCESSION BX359829
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1092)
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6269.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI062AD12QF1&cluster=6269.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI062AD12QF1.

FEATURES
source

Location/Qualifiers
1. .1092
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI062YG23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT 237 a 268 c 322 g 207 t 58 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 13; Length 1092;
Best Local Similarity 95.5%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAACTTGT 25
|||||
Db 36 CAGCTTTTGTACAACTTGT 15

RESULT 11
AL515449/c
LOCUS
DEFINITION AL515449 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
clone CLOBB018ZD09 3-PRIME, mRNA sequence.
ACCESSION AL515449
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1097)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12778942.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3923.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB018ZD09FPI&cluster=3923.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB018ZD09FPI.

FEATURES
source

Location/Qualifiers
1. .1097
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBB018ZD09"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT 250 a 249 c 312 g 249 t 37 others
ORIGIN

Query Match 81.6%; Score 20.4; DB 9; Length 1097;
Best Local Similarity 95.5%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTCTTGTACAACTTGT 25
|||||
Db 39 CAGCTTTTGTACAACTTGT 18

RESULT 12
BX394655/c
LOCUS
DEFINITION BX394655 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CSODC019VE16 5-PRIME, mRNA sequence.
ACCESSION BX394655
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1145)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

```

QY      4 CAGCTTCTTGACAACTTGT 25
Db      36 CTGCTTCTTGACAACTTGT 15

RESULT 7
BG775435      821 bp      mRNA      linear      EST 15-MAY-2001
DEFINITION    602649914T1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4760955 3',
              mRNA sequence.
ACCESSION     BG775435
VERSION       BG775435.1 GI:14045752
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

REFERENCE     1 (bases 1 to 821)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              Tissue Procurement: DCTP/DTP
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLC1612 row: k column: 04
              High quality sequence start: 2
              High quality sequence stop: 816.
              Location/Qualifiers
FEATURES     source
              1..821
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4760955"
                /tissue_type="carcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: prostate; Vector: pOT7; Site 1: XhoI;
                Site 2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH MGC Library."
BASE COUNT   202 a 200 c 214 g 205 t
ORIGIN
Query Match      81.6%; Score 20.4; DB 12; Length 821;
Best Local Similarity 95.8%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CAGCTTCTTGACAACTTGT 25
Db      735 CTGCTTCTTGACAACTTGT 756

RESULT 8
AL536575/c      917 bp      mRNA      linear      EST 31-MAY-2003
LOCUS          AL536575
DEFINITION     AL536575 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
              CS0DF038YL18 5-PRIME, mRNA sequence.
ACCESSION     AL536575
VERSION       AL536575.2 GI:31261203
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

Query Match      81.6%; Score 20.4; DB 12; Length 821;
Best Local Similarity 95.8%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 917)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12800068.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2189.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF038DF09Q1&cluster=2189.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF038DF09Q1.
Location/Qualifiers
1..917
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF038YL18"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 230 a 214 c 222 g 240 t 11 others
ORIGIN

FEATURES
source

Query Match 81.6%; Score 20.4; DB 9; Length 917;
Best Local Similarity 95.5%; Pred. No. 4.1e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CAGCTTCTTGACAACTTGT 25
Db 32 CAGCTTCTTGACAACTTGT 11
RESULT 9
BX441089/c
LOCUS BX441089
DEFINITION BX441089 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF014YA08 5-PRIME, mRNA sequence.
ACCESSION BX441089
VERSION BX441089.1 GI:30789927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 934)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2850.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF014BA04Q1&cluster=2850.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF014BA04Q1.

A protein-protein interaction map of the Caenorhabditis elegans 26S

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

EMBO Rep. 2 (9), 821-828 (2001)
21443405

11559592

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Trace dvpl6v51.x with Bait unknown

POLYA=No.

FEATURES

source

Location/Qualifiers

1..598
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmCDNA"

/note="The AD-wrmCDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 169 a 139 c 146 g 144 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 598;

Best Local Similarity 95.5%; Pred. No. 3.7e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25

| | | | | | | | | | | | | | | | | | | | | |

Db 106 CTGCTTTCTTGTACAAACTTGT 85

RESULT 5

CB104084/c

LOCUS

ADP SQ01509f6 AD-wrmCDNA Caenorhabditis elegans cDNA, mRNA sequence. EST 28-JAN-2003

DEFINITION

CB104084

ACCESSION

CB104084.1 GI:27929891

VERSION

EST.

KEYWORDS

SOURCE

Caenorhabditis elegans

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

REFERENCE

AUTHORS

1 (bases 1 to 668)

Davy, A., Bello, P., Thierry-Mieg, N., Vaglio, P., Hitti, J.,

Doucette-Stamm, L., Thierry-Mieg, D., Reboul, J., Boulton, S., Walhout

A.J., Coux, O. and Vidal, M.

TITLE

A protein-protein interaction map of the Caenorhabditis elegans 26S

proteasome

EMBO Rep. 2 (9), 821-828 (2001)

JOURNAL

21443405

MEDLINE

PUBMED

11559592

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Trace dvpl6v66.x with Bait unknown

POLYA=No.

FEATURES

source

Location/Qualifiers

1..668
/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmCDNA"

/note="The AD-wrmCDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 188 a 159 c 181 g 140 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 14; Length 668;

Best Local Similarity 95.5%; Pred. No. 3.8e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCTTGTACAAACTTGT 25

| | | | | | | | | | | | | | | | | | | | | |

Db 106 CTGCTTTCTTGTACAAACTTGT 85

RESULT 6

AL557510/c

LOCUS

AL557510 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA

DEFINITION

clone CS0DH006YE16 5-PRIME, mRNA sequence.

ACCESSION

AL557510

VERSION

AL557510.2 GI:31279310

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 801)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12901183.

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

5973.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DH006BC08QPI&cluster=5973.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DH006BC08QPI.

Location/Qualifiers

1..801

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="CS0DH006YE16"

/tissue_type="T CELLS (JURKAT CELL LINE)"

/cell_line="JURKAT CELL LINE"

/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"

/note="Vector: pCMVSPORT6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

BASE COUNT 268 a 158 c 249 g 119 t

ORIGIN

Query Match 81.6%; Score 20.4; DB 9; Length 801;

Best Local Similarity 95.5%; Pred. No. 4e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 22:08:13 ; Search time 1093.75 Seconds
(without alignments)
555.531 Million cell updates/sec

Title: US-10-055-001A-5

Perfect score: 25

Sequence: 1 gttcagctttctgtacaacttgt 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vit:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	21.2	84.8	1201	13 BX376823	BX376823 BX376823
c 2	20.8	83.2	996	13 BX329816	BX329816 BX329816
c 3	20.4	81.6	559	9 AL515389	AL515389 AL515389
c 4	20.4	81.6	598	14 CB104071	CB104071 ADP_SQ015

c 5	20.4	81.6	668	14 CB104084	CB104084 ADP_SQ015
c 6	20.4	81.6	801	9 AL557510	AL557510 AL557510
c 7	20.4	81.6	821	12 BG775435	BG775435 602649914
c 8	20.4	81.6	917	9 AL536575	AL536575 AL536575
c 9	20.4	81.6	934	13 BX441089	BX441089 BX441089
c 10	20.4	81.6	1092	13 BX359829	BX359829 BX359829
c 11	20.4	81.6	1097	9 AL515449	AL515449 AL515449
c 12	20.4	81.6	1145	13 BX394655	BX394655 BX394655
c 13	20.4	81.6	1201	13 BX361644	BX361644 BX361644
c 14	20.2	80.8	645	12 BI858895	BI858895 603389227
c 15	20.2	80.8	706	10 BG573114	BG573114 602594115
c 16	20.2	80.8	812	10 BF695849	BF695849 601852207
c 17	20.2	80.8	817	12 BF547007	BF547007 603190329
c 18	20.2	80.8	884	10 BF669965	BF669965 602118471
c 19	20.2	80.8	914	9 AL519260	AL519260 AL519260
c 20	20.2	80.8	956	13 BX457051	BX457051 BX457051
c 21	20.2	80.8	973	13 BX422399	BX422399 BX422399
c 22	20.2	80.8	991	13 BX345037	BX345037 BX345037
c 23	20.2	80.8	1006	13 BX428996	BX428996 BX428996
c 24	20.2	80.8	894	13 BX333971	BX333971 BX333971
c 25	20.2	80.8	897	9 AL538354	AL538354 AL538354
c 26	20.2	80.8	910	13 BX395287	BX395287 BX395287
c 27	20.2	80.8	933	13 BX334648	BX334648 BX334648
c 28	20.2	80.8	959	9 AL514767	AL514767 AL514767
c 29	20.2	80.8	1060	9 AL550767	AL550767 AL550767
c 30	20.2	80.8	1084	13 BX338865	BX338865 BX338865
c 31	20.2	80.8	1190	13 BX374761	BX374761 BX374761
c 32	20.2	80.8	1198	13 BX463747	BX463747 BX463747
c 33	20.2	80.8	1201	9 AL513677	AL513677 AL513677
c 34	20.2	80.8	1201	9 AL514171	AL514171 AL514171
c 35	20.2	80.8	1201	9 AL544923	AL544923 AL544923
c 36	20.2	80.8	1201	9 AL554071	AL554071 AL554071
c 37	20.2	80.8	1201	13 BX363509	BX363509 BX363509
c 38	20.2	80.8	1201	13 BX382731	BX382731 BX382731
c 39	20.2	80.8	1201	13 BX386369	BX386369 BX386369
c 40	20.2	80.8	1201	13 BX400983	BX400983 BX400983
c 41	20.2	80.8	1201	13 BX463202	BX463202 BX463202
c 42	19.8	79.2	402	12 BM953409	BM953409 952062A07
c 43	19.8	79.2	427	10 BG410582	BG410582 947050F08
c 44	19.8	79.2	436	13 BQ163507	BQ163507 952079D01
c 45	19.8	79.2	459	13 BQ163217	BQ163217 952079D01

ALIGNMENTS

RESULT 1	BX376823/c	BX376823	Homo sapiens	1201 bp	mRNA	linear	EST 08-MAY-2003
LOCUS	BX376823	Homo sapiens	NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens				
DEFINITION	CDNA clone CS0DD006YE08 5-PRIME, mRNA sequence.						
ACCESSION	BX376823						
VERSION	BX376823.1	GI:30442822					
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 1201)						
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.						
TITLE	Full-length cDNA libraries and normalization						
JOURNAL	Unpublished						
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2992.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DD006BC04QPI&cluster=2992.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600						

```
RESULT 38
US-09-732-914-45/C
; Sequence 45, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 43
; TYPE: DNA
; ORGANISM: attR2 PCR Primer
US-09-732-914-45

Query Match          93.6%; Score 23.4; DB 9; Length 43;
Best Local Similarity 96.0%; Pred. No. 1.6;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
Db 29 GTTCAGCTTTCCTGACAAACTTGT 5
```

```
RESULT 39
US-09-855-797A-42
; Sequence 42, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-42

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25
```

```
RESULT 40
US-09-907-900-42
; Sequence 42, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-42

Query Match          90.4%; Score 22.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
Db 1 GTTCAGCTTTTGTGACAAACTTGT 25
```

```
Search completed: November 7, 2003, 02:22:25
Job time : 103.25 secs
```

```

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
; INFORMATION FOR SEQ ID NO: 10:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MISMATCHES: 0; Mismatches 1; Indels 0; Gaps 0;
;
; QUERY MATCH
; BEST LOCAL SIMILARITY 93.6%; Score 23.4; DB 14; Length 25;
; MATCHES 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTTTGTACAAACTTGT 25
; DB 1 GTTCAGCTTTTGTACAAACTTGT 25
;
; RESULT 36
; US-10-162-879-10
; Sequence 10, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brach, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002

```

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
; US-10-162-879-10
;
; QUERY MATCH
; BEST LOCAL SIMILARITY 93.6%; Score 23.4; DB 14; Length 25;
; MATCHES 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTTTGTACAAACTTGT 25
; DB 1 GTTCAGCTTTTGTACAAACTTGT 25
;
; RESULT 37
; US-10-161-403-50
; Sequence 50, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attr2
; US-10-161-403-50
;
; QUERY MATCH
; BEST LOCAL SIMILARITY 93.6%; Score 23.4; DB 14; Length 25;
; MATCHES 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GTTCAGCTTTTGTACAAACTTGT 25
; DB 1 GTTCAGCTTTTGTACAAACTTGT 25

```

```
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-432-085-10

Query Match          93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 32
US-09-985-448-10
; Sequence 10, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-10

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 33
US-10-300-892-10
; Sequence 10, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
```

```
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-10

Query Match          93.6%; Score 23.4; DB 12; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 34
US-10-055-001A-5
; Sequence 5, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: core sequence of recombination site attr2
US-10-055-001A-5

Query Match          93.6%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
   |||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 35
US-10-058-292-10
; Sequence 10, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
```

RESULT 28
US-09-855-797A-10
; Sequence 10, Application US/09855797A
; Patent No. US2002094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-10

Query Match 93.6%; Score 23.4; DB 9; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 29
US-09-907-900-10
; Sequence 10, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-10

Query Match 93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 30
US-09-907-719-10
; Sequence 10, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-10

Query Match 93.6%; Score 23.4; DB 10; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTCTGTACAAACTTGT 25

RESULT 31
US-09-432-085-10
; Sequence 10, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match      100.0%; Score 25; DB 12; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 24
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match      100.0%; Score 25; DB 14; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 25
US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match      100.0%; Score 25; DB 14; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 16674 GTTCAGCTTTTGTACAAACTTGT 16698

RESULT 26
US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match      100.0%; Score 25; DB 14; Length 17681;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026

RESULT 27
US-10-055-001A-26/c
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match      100.0%; Score 25; DB 14; Length 17681;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 13050 GTTCAGCTTTTGTACAAACTTGT 13026
```

```
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 581
; LENGTH: 11180
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-581
```

```
Query Match 100.0%; Score 25; DB 10; Length 11180;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
DB 142 GTTCAGCTTTTGTACAAACTTGT 118
```

```
RESULT 20
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25
```

```
Query Match 100.0%; Score 25; DB 14; Length 17458;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
DB 16656 GTTCAGCTTTTGTACAAACTTGT 16680
```

```
RESULT 21
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
```

```
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25
```

```
Query Match 100.0%; Score 25; DB 14; Length 17458;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
DB 13050 GTTCAGCTTTTGTACAAACTTGT 13026
```

```
RESULT 22
US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7
```

```
Query Match 100.0%; Score 25; DB 12; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
DB 16674 GTTCAGCTTTTGTACAAACTTGT 16698
```

```
RESULT 23
US-10-385-546-7/c
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
```



```
; FILE REFERENCE: A-70174-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/023,208
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,163
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-023-208-63

Query Match      100.0%; Score 25; DB 14; Length 1846;
Best Local Similarity 100.0%; Pred. No. 0.64; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY      1 GTTCAGCTTTTGTACAAACTTGT 25
Db      25 GTTCAGCTTTTGTACAAACTTGT 1

RESULT 17
US-10-241-596-137/c
; Sequence 137, Application US/10241596
; Publication No. US20030166238A1
; GENERAL INFORMATION:
; APPLICANT: Microbiological Research Authority
; APPLICANT: The Speywood Laboratory Limited
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130003
; CURRENT APPLICATION NUMBER: US/10/241,596
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: US 09/242,689
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB 9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB 9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 5558
; TYPE: DNA
; ORGANISM: Clostridium botulinum
US-10-241-596-137

Query Match      100.0%; Score 25; DB 12; Length 5558;
Best Local Similarity 100.0%; Pred. No. 0.78; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY      1 GTTCAGCTTTTGTACAAACTTGT 25
Db      1666 GTTCAGCTTTTGTACAAACTTGT 1642

RESULT 18
US-10-151-690-20/c
; Sequence 20, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPPOSITO, DOMINIC
```

```
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 6464
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDEST1
; NAME/KEY: gene
; LOCATION: (216)..(257)
; OTHER INFORMATION: Trc promoter
; NAME/KEY: gene
; LOCATION: (273)..(393)
; OTHER INFORMATION: attR1
; NAME/KEY: gene
; LOCATION: (647)..(1306)
; OTHER INFORMATION: Cmr
; NAME/KEY: gene
; LOCATION: (1426)..(1510)
; OTHER INFORMATION: inactivated ccdA
; NAME/KEY: gene
; LOCATION: (1648)..(1953)
; OTHER INFORMATION: ccdB
; NAME/KEY: gene
; LOCATION: (1994)..(2118)
; OTHER INFORMATION: attR2
; NAME/KEY: gene
; LOCATION: (2598)..(3503)
; OTHER INFORMATION: ampr
; NAME/KEY: gene
; LOCATION: (4104)..(4264)
; OTHER INFORMATION: ori
; NAME/KEY: gene
; LOCATION: (4504)..(4941)
; OTHER INFORMATION: flori (fl intergenic region)
; NAME/KEY: gene
; LOCATION: (5340)..(6420)
; OTHER INFORMATION: lacIq
US-10-151-690-20

Query Match      100.0%; Score 25; DB 14; Length 6464;
Best Local Similarity 100.0%; Pred. No. 0.8; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY      1 GTTCAGCTTTTGTACAAACTTGT 25
Db      297 GTTCAGCTTTTGTACAAACTTGT 273

RESULT 19
US-09-887-576-581/c
; Sequence 581, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
```

; Sequence 32, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attR1
US-10-151-690-32

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 13
US-09-974-760B-33/c
; Sequence 33, Application US/09974760B
; Publication No. US20030143705A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Shannon
; APPLICANT: Sherman, Amir
; APPLICANT: Trueheart, Joshua
; APPLICANT: Milne, G. Todd
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES
; FILE REFERENCE: 14184-009001
; CURRENT APPLICATION NUMBER: US/09/974,760B
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-974-760B-33

Query Match 100.0%; Score 25; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 14
US-09-732-914-44/c
; Sequence 44, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.

; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 43
; TYPE: DNA
; ORGANISM: attR1 PCR Primer
US-09-732-914-44

Query Match 100.0%; Score 25; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTTCAGCTTTTGTACAAACTTGT 5

RESULT 15
US-10-151-690-19/c
; Sequence 19, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDEST1
US-10-151-690-19

Query Match 100.0%; Score 25; DB 14; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 118 GTTCAGCTTTTGTACAAACTTGT 94

RESULT 16
US-10-023-208-63/c
; Sequence 63, Application US/10023208
; Publication No. US20030124537A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; APPLICANT: Liu, Yuan-Ching
; TITLE OF INVENTION: PROCARYOTIC LIBRARIES AND USES

```
/
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/10/058,292
/ FILING DATE: 30-Jan-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/432,085
/ FILING DATE: 1999-11-02
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-058-292-9

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 10
US-10-162-879-9
; Sequence 9, Application US/10162879
; Publication No. US20030086799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Braesch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/162,879
/ FILING DATE: 06-Jun-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,085
```

```
/
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-162-879-9

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 11
US-10-161-403-49
; Sequence 49, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attr1
US-10-161-403-49

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 12
US-10-151-690-32
```

APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-432-085-9

Query Match 100.0%; Score 25; DB 11; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 6

US-09-985-448-9
Sequence 9, Application US/09985448
Publication No. US20030157716A1

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/985,448
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: US 60/065,930
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-985-448-9

Query Match 100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 7

US-10-300-892-9
Sequence 9, Application US/10300892
Publication No. US20030175970A1

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/10/300,892
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/907,719
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
US-10-300-892-9

Query Match 100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 8

US-10-055-001A-4
Sequence 4, Application US/10055001A
Publication No. US20030049835A1

GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
FILE REFERENCE: HELIGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: core sequence of recombination site attr1
US-10-055-001A-4

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 9

US-10-058-292-9
Sequence 9, Application US/10058292
Publication No. US20030054552A1

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington

; Patent No. US2002009457AA1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-9

Query Match 100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
DB 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 3
US-09-907-900-9
; Sequence 9, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-9

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
DB 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 4
US-09-907-719-9

; Sequence 9, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-9

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
DB 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 5
US-09-432-085-9
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 23:06:49 ; Search time 102.25 Seconds
(without alignments)
780.185 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaactgt 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2141354 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	9	US-09-732-914-8
2	25	100.0	25	9	US-09-855-797A-9
3	25	100.0	25	10	US-09-907-900-9
4	25	100.0	25	10	US-09-907-719-9
5	25	100.0	25	11	US-09-432-085-9
6	25	100.0	25	12	US-09-985-448-9
7	25	100.0	25	12	US-10-300-892-9
8	25	100.0	25	14	US-10-055-001A-4
9	25	100.0	25	14	US-10-058-292-9
10	25	100.0	25	14	US-10-162-879-9
11	25	100.0	25	14	US-10-161-403-49
12	25	100.0	25	14	US-10-151-690-32
13	25	100.0	35	12	US-09-974-760B-33
14	25	100.0	43	9	US-09-732-914-44
15	25	100.0	120	14	US-10-151-690-19
16	25	100.0	1846	14	US-10-023-208-63

c 17	25	100.0	5558	12	US-10-241-596-137	Sequence 137, Appl
c 18	25	100.0	6464	14	US-10-151-690-20	Sequence 20, Appl
c 19	25	100.0	11180	10	US-09-887-576-591	Sequence 581, Appl
c 20	25	100.0	17458	14	US-10-055-001A-25	Sequence 25, Appl
c 21	25	100.0	17458	14	US-10-055-001A-25	Sequence 25, Appl
c 22	25	100.0	17476	12	US-10-385-546-7	Sequence 7, Appl
c 23	25	100.0	17476	12	US-10-385-546-7	Sequence 7, Appl
c 24	25	100.0	17476	14	US-10-055-001A-24	Sequence 24, Appl
c 25	25	100.0	17476	14	US-10-055-001A-24	Sequence 24, Appl
c 26	25	100.0	17681	14	US-10-055-001A-26	Sequence 26, Appl
c 27	25	100.0	17681	14	US-10-055-001A-26	Sequence 26, Appl
c 28	23.4	93.6	25	9	US-09-855-797A-10	Sequence 10, Appl
c 29	23.4	93.6	25	10	US-09-907-900-10	Sequence 10, Appl
c 30	23.4	93.6	25	10	US-09-907-900-10	Sequence 10, Appl
c 31	23.4	93.6	25	11	US-09-432-085-10	Sequence 10, Appl
c 32	23.4	93.6	25	12	US-09-985-448-10	Sequence 10, Appl
c 33	23.4	93.6	25	12	US-10-300-892-10	Sequence 10, Appl
c 34	23.4	93.6	25	14	US-10-058-292-10	Sequence 5, Appl
c 35	23.4	93.6	25	14	US-10-058-292-10	Sequence 10, Appl
c 36	23.4	93.6	25	14	US-10-162-879-10	Sequence 10, Appl
c 37	23.4	93.6	25	14	US-10-161-403-50	Sequence 50, Appl
c 38	23.4	93.6	43	9	US-09-732-914-45	Sequence 45, Appl
c 39	22.6	90.4	25	9	US-09-855-797A-42	Sequence 42, Appl
c 40	22.6	90.4	25	10	US-09-907-900-42	Sequence 42, Appl
c 41	22.6	90.4	25	10	US-09-907-900-42	Sequence 42, Appl
c 42	22.6	90.4	25	12	US-09-985-448-42	Sequence 42, Appl
c 43	22.6	90.4	25	12	US-10-300-892-42	Sequence 42, Appl
c 44	22.4	89.6	25	9	US-09-855-797A-15	Sequence 15, Appl
c 45	22.4	89.6	25	10	US-09-907-900-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-732-914-8
; Sequence 8, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James D.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr1
US-09-732-914-8

Query Match 100.0%; Score 25; DB 9; Length 25;
Best local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTGT 25

Db 1 GTTCAGCTTTTGTACAACTGT 25

RESULT 2

US-09-855-797A-9
; Sequence 9, Application US/09855797A

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25

Db 166 GTTCAGCTTTTGTACAAACTTGT 142

Search completed: November 6, 2003, 22:26:28
Job time : 112.5 secs

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 4022 GTTCAGCTTTTGTACAACTTGT 3998

RESULT 39
 AAC55464/C
 ID AAC55464 standard; DNA; 5957 BP.
 XX
 AC AAC55464;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST5 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 FN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 15; Fig 25; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 5957 BP; 1509 A; 1443 C; 1498 G; 1507 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5957;
 Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 205 GTTCAGCTTTTGTACAACTTGT 181

RESULT 40
 AAC55467/C
 ID AAC55467 standard; DNA; 5957 BP.
 XX
 AC AAC55467;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST6 nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 FN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 15; Fig 26; 459pp; English.
 XX
 CC The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 5957 BP; 1530 A; 1445 C; 1496 G; 1486 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5957;
 Best Local Similarity 100.0%; Pred. No. 0.48;

CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 4554 BP; 1194 A; 1070 C; 1113 G; 1177 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 4554;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
DB 310 GTTCAGCTTTTGTACAAACTTGT 286

RESULT 37
AAD27063/c
ID AAD27063 standard; DNA; 5148 BP.
AC AAD27063;
XX
DT 09-APR-2002 (first entry)
XX
DE Plasmid pGN39 DNA.
XX
KW Vector construct; RNA inhibition; RNAi; gene expression control;
KW pGN39 plasmid; ds.
XX
OS Unidentified.
XX
FN WO200188121-A1.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-IB01068.
XX
PR 19-MAY-2000; 2000GB-0012233.
XX
PA (DEVG-) DEVGEN NV.
XX
PI Plaetinck G, Renard J, Bogaert T;
XX
DR WPI; 2002-121984/16.

CC A new DNA vector construct containing opposable promoter and terminator
CC sequences flanking a cloning site are useful for the expression of
CC double stranded RNA useful for inhibition of RNA in gene expression
CC control -
XX
PS Claim 24; Fig 12; 75pp; English.

CC The present invention relates to improved vector constructs comprising
CC two promoters in opposite orientation to each other, an inter-promoter
CC region downstream of the 3' end of both promoters, a cloning site in
CC the inter-promoter region and a transcription terminator downstream
CC of the 3' end of the first promoter and the cloning site and operably
CC linked to the first promoter. The constructs of the invention and the
CC bacteria harbouring the constructs are used to produce double stranded
CC RNA for RNA inhibition (RNAi) and can be used as a tool for controlling
CC gene expression. The present sequence is pGN39 plasmid DNA.
XX
SQ Sequence 5148 BP; 1359 A; 1199 C; 1279 G; 1311 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 5148;
Best Local Similarity 100.0%; Pred. No. 0.47;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
DB 171 GTTCAGCTTTTGTACAAACTTGT 147
RESULT 38
AAC55481/c
ID AAC55481 standard; DNA; 5848 BP.
XX
AC AAC55481;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST13 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attL; attR;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
FN WO2000052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.

CC Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
CC attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
CC recombinational cloning of polypeptides -
XX
PS Disclosure; Fig 33; 459pp; English.

CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 5848 BP; 1563 A; 1364 C; 1379 G; 1542 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 5848;
Best Local Similarity 100.0%; Pred. No. 0.48;

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (i), (ii), (iii), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (i), (ii), (iii), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 420 BP; 134 A; 77 C; 88 G; 121 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 420;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 402 GTTCAGCTTTTGTACAACTTGT 378

RESULT 35

AAD44626/C
 ID AAD44626 standard; DNA; 1846 BP.

XX AC

XX AC

XX AC

DT 13-DEC-2002 (first entry)

XX Gateway transfer cassette DNA.

XX Prokaryotic library; candidate protein; nucleic acid modification; NAM;
 KW enzyme attachment sequence; EAS; clinical pharmacology; chemical sensor;
 KW enzymology; cosmetic research; toxic; environmental safety assessment;
 KW nutrient biology; gateway transfer cassette; gene; ds.

XX Unidentified.

XX WO200266653-A2.

XX 29-AUG-2002.

XX 14-DEC-2001; 2001WO-US49058.

XX 14-DEC-2000; 2000US-256163P.

XX (XENC-) XENCOR INC.

XX Li M, Liu Y;

XX WPI; 2002-667068/71.

XX New library of prokaryotic pET-24a expression vectors, host cells or
 PT nucleic acid/protein conjugates, useful for screening candidate
 PT proteins and their nucleic acids or modification enzymes for
 PT pharmacogenetic analysis -

XX Example 2; Fig 59B; 127pp; English.

XX The invention relates to methods and compositions for the construction
 CC of prokaryotic libraries expressing candidate proteins and the use of
 CC these libraries to identify candidate proteins and the nucleic acids
 CC encoding them. The invention provides a library of prokaryotic pET-24a
 CC vectors comprising a fusion nucleic acid consisting of a nucleic acid
 CC encoding a nucleic acid modification (NAM) enzyme or a candidate
 CC protein, or a nucleic acid having a T7 promoter operably linked to the
 CC NAM enzyme or the candidate protein, and an enzyme attachment sequence
 CC (EAS) recognised by the NAM enzyme. The library is used for identifying

CC candidate proteins and nucleic acids encoding these proteins, in
 CC screening for NAM enzymes with decreased toxicity for the host cells,
 CC or in identifying novel or improved EASs, which may be used for
 CC understanding cellular processes or any subsequent therapeutic or toxic
 CC activities. The nucleic acid/protein (NAP) conjugates are useful in
 CC diagnostic assays and in research including clinical pharmacology,
 CC functional genomics, pharmacogenomics, agricultural chemicals,
 CC environmental safety assessment, chemical sensor, nutrient biology,
 CC cosmetic research or enzymology. These may also be used in vitro
 CC screening techniques and in assays with target molecules. The present
 CC sequence is gateway transfer cassette DNA used in the invention.

XX Sequence 1846 BP; 527 A; 381 C; 434 G; 504 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 1846;

Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 25 GTTCAGCTTTTGTACAACTTGT 1

RESULT 36

AAC55541/C

ID AAC55541 standard; DNA; 4554 BP.

XX AC

XX AC

XX AC

DT 11-JAN-2001 (first entry)

XX attR reading frame C parent plasmid pRfC Parent III nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attL; attR2;

KW mutant; recombinational cloning; entry vector; destination vector;

KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 14; Fig 83; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 306 BP; 87 A; 77 C; 80 G; 62 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 306;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 301 GTTCAGCTTTTGTACAACTTGT 277

RESULT 33
 AAC5514/c
 ID AAC5514 standard; DNA; 306 BP.

XX AAC5514;

XX 11-JAN-2001 (first entry)

DE Destination vector pDBST26 fragment nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
 OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Disclosure; Fig 46; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 306 BP; 84 A; 83 C; 74 G; 65 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 306;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 301 GTTCAGCTTTTGTACAACTTGT 277

RESULT 34
 AAC55492/c
 ID AAC55492 standard; DNA; 420 BP.

XX AAC55492;

XX 11-JAN-2001 (first entry)

DE Destination vector pDBST18 fragment nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.
 OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Disclosure; Fig 38; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 255 BP; 88 A; 57 C; 50 G; 60 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 255;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 Db 253 GTTCAGCTTTTGTACAAACTTGT 229

RESULT 31
 AAC55478/c
 ID AAC55478 standard; DNA; 255 BP.

XX AC AAC55478;

XX 11-JAN-2001 (first entry)

DE Destination vector pDEST12 fragment nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 15; Fig 32; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 255 BP; 80 A; 67 C; 58 G; 50 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 255;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 Db 235 GTTCAGCTTTTGTACAAACTTGT 211

RESULT 32

AAC55468/c

ID AAC55468 standard; DNA; 306 BP.

XX AC AAC55468;

XX 11-JAN-2001 (first entry)

DE Destination vector pDEST7 fragment nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 15; Fig 27; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 204 BP; 80 A; 35 C; 31 G; 58 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 Db 184 GTTCAGCTTTTGTACAAACTTGT 160

RESULT 29
 AAC55476/c
 ID AAC55476 standard; DNA; 204 BP.
 XX
 AC AAC55476;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST11 fragment nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Synthetic.
 XX WO200052027-A1.
 XX
 XX 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 XX 02-MAR-1999; 99US-0122389.
 XX 23-MAR-1999; 99US-0126049.
 XX 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX
 XX Example 13; Fig 31; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising att

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 204 BP; 60 A; 53 C; 50 G; 41 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 Db 181 GTTCAGCTTTTGTACAAACTTGT 157

RESULT 30
 AAC55460/c
 ID AAC55460 standard; DNA; 255 BP.
 XX
 AC AAC55460;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE His6-Trx expression cassette for destination vector pDEST4.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Escherichia coli.
 XX WO200052027-A1.
 XX
 XX 08-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05432.
 XX
 XX 02-MAR-1999; 99US-0122389.
 XX 23-MAR-1999; 99US-0126049.
 XX 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 XX recombinational cloning of polypeptides -
 XX
 XX Disclosure; Fig 24; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising att

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 153 BP; 50 A; 28 C; 40 G; 35 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 DB 127 GTTCAGCTTTTGTACAAACTTGT 103

RESULT 27
 AAC55465/c
 ID AAC55465 standard; DNA; 204 BP.
 XX
 AC AAC55465;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pBEST6 fragment nucleotide sequence #1.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.

PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.
 XX
 PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Example 15; Fig 26; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 204 BP; 70 A; 40 C; 46 G; 48 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 |||||
 DB 166 GTTCAGCTTTTGTACAAACTTGT 142

RESULT 28
 AAC55470/c
 ID AAC55470 standard; DNA; 204 BP.
 XX
 AC AAC55470;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Destination vector pBEST8 fragment nucleotide sequence.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.

OS Bacteriophage lambda.
 OS Synthetic.
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX
 DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX

PS Example 15; Fig 28; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 125 BP; 61 A; 18 C; 14 G; 32 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 125;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 25 GTTCAGCTTTTGTACAACTTGT 1

RESULT 25
 AAC55485/c
 ID AAC55485 standard; DNA; 153 BP.
 XX
 AC AAC55485;
 XX
 XX 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST15 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attL; attR;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 35; 453pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising att

CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III), primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing vectors, targeting
 CC gene products to intracellular locations, cleaving fusion tags from
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 153 BP; 52 A; 29 C; 33 G; 39 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 153;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 DB 103 GTTCAGCTTTTGTACAACTTGT 79

RESULT 26
 AAC55488/c
 ID AAC55488 standard; DNA; 153 BP.
 XX
 AC AAC55488;
 XX
 XX 11-JAN-2001 (first entry)
 XX
 DE Destination vector pDEST16 fragment nucleotide sequence #2.
 XX
 KW Bacteriophage lambda; att; recombination site; attB; attP; attL;
 KW mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; ds.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200052027-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05432.
 XX
 PR 02-MAR-1999; 99US-0122389.
 PR 23-MAR-1999; 99US-0126049.
 PR 28-MAY-1999; 99US-0136744.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;
 XX WPI; 2000-543948/49.
 XX
 XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -
 XX
 PS Disclosure; Fig 36; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
 CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising att

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (i), (ii), (iii), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (i), (ii), (iii), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 102 BP; 37 A; 24 C; 19 G; 21 T; 1 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 92 GTTCAGCTTTTGTACAACTTGT 68

RESULT 23
AAC55453/c
ID AAC55453 standard; DNA; 120 BP.

XX AC AAC55453;

XX DT 11-JAN-2001 (first entry)

XX DE Trc expression cassette for destination vector pDEST1.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.
XX OS Escherichia coli.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Disclosure; Fig 21; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (i)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (ii) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (iii)
XX CC comprising one or more mutated att recombination sites comprising at

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (i), (ii), (iii), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (i), (ii), (iii), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 120 BP; 44 A; 19 C; 28 G; 29 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 118 GTTCAGCTTTTGTACAACTTGT 94

RESULT 24

AAC55384/c

ID AAC55384 standard; DNA; 125 BP.

XX AC AAC55384;

XX DT 11-JAN-2001 (first entry)

XX DE Recombination site nucleotide sequence attR1.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05432.

XX PR 02-MAR-1999; 99US-0122389.

XX PR 23-MAR-1999; 99US-0126049.

XX PR 28-MAY-1999; 99US-0136744.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides -
XX PS Claim 1; Fig 9; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (i)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (ii) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (iii)
XX CC comprising one or more mutated att recombination sites comprising at

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 102 BP; 40 A; 22 C; 18 G; 22 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
Db 83 GTTCAGCTTTTGTACAACTTGT 59

RESULT 21
AAC55508/c
ID AAC55508 standard; DNA; 102 BP.
XX AAC55508;
AC AAC55508;
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST24 fragment nucleotide sequence #1.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Example 5; Fig 44; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing fusion tags, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 102 BP; 37 A; 25 C; 19 G; 21 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAACTTGT 25
Db 95 GTTCAGCTTTTGTACAACTTGT 71

RESULT 22
AAC55511/c
ID AAC55511 standard; DNA; 102 BP.
XX AAC55511;
AC AAC55511;
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST25 fragment nucleotide sequence #1.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Example 5; Fig 45; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 35 A; 19 C; 20 G; 28 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 70 GTTCAGCTTTTGTACAACTTGT 46

RESULT 19
AAC55500/c
ID AAC55500 standard; DNA; 102 BP.
XX AAC55500;
AC AAC55500;
XX
DT 11-JAN-2001 (first entry)
XX Destination vector pBEST21 fragment nucleotide sequence #2.
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
OS
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
PT
XX Disclosure; Fig 41; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX Sequence 102 BP; 45 A; 13 C; 24 G; 20 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 82 GTTCAGCTTTTGTACAACTTGT 58

RESULT 20
AAC55505/c
ID AAC55505 standard; DNA; 102 BP.
XX AAC55505;
AC AAC55505;
XX
DT 11-JAN-2001 (first entry)
XX Destination vector pDEST23 fragment nucleotide sequence #1.
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
OS
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05432.
XX
XX 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
PT
XX Example 5; Fig 43; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 87 BP; 26 A; 19 C; 21 G; 21 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 79 GTTCAGCTTTTGTACAAACTTGT 55

RESULT 17
AAC55497/c
ID AAC55497 standard; DNA; 95 BP.
XX
AC AAC55497;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST20 fragment nucleotide sequence #2.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI
XX WPI; 2000-543948/49.
DR

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX
PS Example 23; Fig 40; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 95 BP; 41 A; 13 C; 15 G; 26 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 52 GTTCAGCTTTTGTACAAACTTGT 28

RESULT 18
AAC55458/c
ID AAC55458 standard; DNA; 102 BP.
XX
AC AAC55458;
XX
DT 11-JAN-2001 (first entry)
XX
DE GST expression cassette for destination vector pDEST3 #2.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Escherichia coli.
XX
FN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI
XX WPI; 2000-543948/49.
DR

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
XX
PS Example 15; Fig 23; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)

XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination
CC site nucleic acid sequences, and PCR primers of the invention. The
CC site sequences are recognised by the recombination protein lambda
CC integrase (Int). The invention is a new method of producing a population
CC of hybrid nucleic acids comprising mixing at least a first population of
CC nucleic acids comprising one or more recombination sites with at least
CC one target nucleic acid comprising one or more recombination sites and
CC causing some or all of the nucleic acids to recombine with all or some of
CC the target nucleic acids. The method is useful for producing a population
CC of hybrid nucleic acids which may be the same or different. The nucleic
CC acids may be used to express therapeutic proteins or peptides and they
CC may also be used to create novel fusion proteins by expressing different
CC sequences linked to each other. The method allows simultaneous cloning of
CC two or more different nucleic acids.

XX SQ Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 29 GTTCAGCTTTTGTACAACTTGT 5

RESULT 15
AAC55503/c
ID AAC55503 standard; DNA; 82 BP.

XX AAC55503;
AC AAC55503;
XX 11-JAN-2001 (first entry)

DE Destination vector pEST22 fragment nucleotide sequence #2.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX MPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides -

XX Disclosure; Fig 42; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)

CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (II), (III), (IV), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX SQ Sequence 82 BP; 39 A; 16 C; 17 G; 10 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCAGCTTTTGTACAACTTGT 25
DB 70 GTTCAGCTTTTGTACAACTTGT 46

RESULT 16

AAC55517/c

ID AAC55517 standard; DNA; 87 BP.

XX AAC55517;

XX 11-JAN-2001 (first entry)

DE Destination vector pEST27 fragment nucleotide sequence #2.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX MPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides -

XX Disclosure; Fig 47; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)

CC metabolite by a fungus. This involves modulating the expression of at
 CC least one ZBC (zinc binuclear cluster protein) gene in a manner to
 CC improve the yield of the secondary metabolite. Methods of the invention
 CC may be used for improving the production of the secondary metabolite e.g.
 CC antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such
 CC as lovastatin or mevastatin), an immunosuppressant (such as cyclosporin A),
 CC an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such
 CC as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds,
 CC a fungal toxin, a modulator of cell surface receptor signalling, a plant
 CC growth regulator, a pigment, an insecticide, or an antineoplastic
 CC compound. The method results in a decrease in fermentor run-time, a
 CC decrease in the size of the fermentor required for the production of
 CC equivalent amounts of the secondary metabolite, or a decrease in the
 CC biomass required for the production, which translates into decreased
 CC waste that must be handled in downstream processing. The sequences given
 CC in record ABL58587-ABL58598 represent primers that are used in
 CC construction of vectors containing the ZBC genes of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 13

AAC55545/c
 ID AAC55545 standard; DNA; 43 BP.

AC AAC55545;

DT 11-JAN-2001 (first entry)

DE att site PCR primer attR1.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
 XX mutant; recombinational cloning; entry vector; destination vector;
 KW gene product targeting; fusion tag cleavage; PCR primer; ss.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US05432.

XX 02-MAR-1999; 99US-0122389.

XX 23-MAR-1999; 99US-0126049.

XX 28-MAY-1999; 99US-0136744.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
 PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
 PT recombinational cloning of polypeptides -

XX Example 19; Page 142; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
 CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
 CC molecule (II) comprising one or more att recombination sites comprising
 CC at least one mutation in its core region that increases the specificity
 CC of interaction between the recombination site and a second att
 CC recombination site; and (2) an isolated nucleic acid molecule (III)
 CC comprising one or more mutated att recombination sites comprising at
 CC least one mutation in its core region that enhances the efficiency of
 CC recombination between a first nucleic acid molecule comprising the
 CC mutated att recombination site and a second nucleic acid molecule
 CC comprising a second recombination site that interacts with the mutated
 CC att recombination site. (I), (II), (III) primers, vectors and methods
 CC from the present invention are used for the recombinational cloning of
 CC nucleic acid molecules. They can be used for changing fusion tags, targeting
 CC gene products to intracellular locations, cleaving fusion tags, forming
 CC desired proteins, operably linking nucleic acid molecules of interest to
 CC regulatory genetic sequences, constructing genes for fusion proteins,
 CC changing copy number, changing replicons, cloning into phages and
 CC cloning. (I), (II), (III), host cells and vectors can be used in the
 CC production of polypeptides and antibodies. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
 Db 29 GTTCAGCTTTTGTACAAACTTGT 5

RESULT 14

AAS06217/c

ID AAS06217 standard; DNA; 43 BP.

AC AAS06217;

DT 12-SEP-2001 (first entry)

DE PCR primer attR1 used to produce a population of hybrid DNA molecules.

XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 XX lambda integrase; therapeutic; ss.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200142509-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33546.

XX 10-DEC-1999; 99US-0169983.

XX 09-MAR-2000; 2000US-0188020.

XX (CHEO/) CHEO D.

XX (BRAS/) BRASCH M A.

XX (TEMP/) TEMPLE G F.

XX (HART/) HARTLEY J L.

XX (BYRD/) BYRD D R N.

XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one
 PT or more recombination sites in the presence of recombination proteins,
 PT e.g. Cre -

XX Example 7; Page 209; 357pp; English.

PS Disclosure; Page 262; 269pp; English.

XX The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention.

XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Query Match 100.0%; Score 25; DB 25; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACGCTTTTGTACAACTTGT 25
 |||||
 DB 1 GTTACGCTTTTGTACAACTTGT 25

RESULT 11

AAH19591/c
 ID AAH19591 standard; DNA; 35 BP.

XX AAH19591;

XX 30-JUL-2001 (first entry)

XX Plasmid pE2C7201 ccdB cassette PCR oligo MO511.

XX Secondary metabolite production; gene expression modulation;
 KW genetically modified fungus; antibacterial; antihypercholesterolaemic;
 KW immunosuppressant; cell surface receptor signalling; pigment;
 KW plant growth regulator; insecticide; anti-neoplastic; ccdB; death gene;
 KW pE2C7201; PCR primer; ss.

XX Unidentified.

XX WO200129073-A1.

XX 26-APR-2001.

XX 18-OCT-2000; 2000WO-US28903.

XX 20-OCT-1999; 99US-0160587.

XX 19-JAN-2000; 2000US-0487358.

XX (MICR-) MICROBIA INC.

XX Busby R, Doten R, Cali B, Hecht P, Holtzman D, Madden K, Maxon M;
 PI Milne T, Norman T, Royer J, Salama S, Sherman A, Silva J;
 PI Summers E, Zhang L, Mayorga M, Feibelman T;

XX WPI; 2001-374304/39.

XX Improving production of secondary metabolite by fungus, for producing
 PT proteins of interest, involves modulating the expression of gene
 PT involved in regulation of secondary metabolite production

XX Example 1; Page 67; 139pp; English.

XX The present sequence is a primer which was used in an example
 CC illustrating an invention relating to a method for improving production
 CC of a secondary metabolite by a fungus. The method involves modulating
 CC the expression of a gene involved in the regulation of secondary
 CC metabolite production. The gene may be modulated in a manner that
 CC increases the yield or productivity of metabolite, increases
 CC efflux or excretion of the metabolite, decreases production of side
 CC effects or competing metabolites, alters the characteristics of the
 CC fungus in a manner that is beneficial to the production of the
 CC metabolite, causes conditional lysis of the fungus, or increases the
 CC resistance of the fungus to deleterious effects of exposure to the
 CC secondary metabolite. The method is useful for producing
 CC genetically modified fungi, which are useful for producing
 CC secondary metabolites such as antibacterial compounds,
 CC antihypercholesterolaemic compounds, immunosuppressants, modulators
 CC of cell surface receptor signalling, plant growth regulators, pigments,
 CC insecticides or anti-neoplastic compounds. The present sequence was
 CC used in the preparation of clones to regulate secondary metabolite
 CC production.

XX SQ Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 35;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACGCTTTTGTACAACTTGT 25
 |||||
 DB 35 GTTACGCTTTTGTACAACTTGT 11

RESULT 12

ABL58593/c

ID ABL58593 standard; DNA; 35 BP.

XX ABL58593;

XX 24-JUL-2002 (first entry)

XX Oligonucleotide MO511.

XX Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein;
 KW antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastatin;
 KW mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine;
 KW angiotensin inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin;
 KW fungal toxin; cell surface receptor; plant growth regulator; pigment;
 KW insecticide; antineoplastic; PCR; primer; ss.

XX Unidentified.

XX WO200224865-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US29288.

XX 19-SEP-2000; 2000US-233564P.

XX (MICR-) MICROBIA INC.

XX Holtzman D, Madden K, Maxon M, Sherman A;

XX WPI; 2002-352005/38.

XX New method for improving the production of a secondary metabolite e.g.
 PT antineoplastic agent, ergot alkaloid from a fungus involves modulation
 PT of the expression of at least one zinc binuclear cluster protein gene

XX Example 1; SEQ ID 7; 49pp + sequence listing; English.

XX The invention relates to improving the production of a secondary

```

PR 30-MAY-2001; 2001US-294758P.
PR 21-MAR-2002; 2002US-366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;
XX
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest -
XX
XX Claim 43; Page 143; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (1) a platform artificial chromosome
CC expression system (ACes) (II) comprising several sites that participate
CC in recombinase catalyzed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of ACes comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96850 to ABP96657 represent sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25
RESULT 9
ABZ58734
ID ABZ58734 standard; DNA; 25 BP.
XX
XX ABZ58734;
AC ABZ58734;
XX
XX 01-MAY-2003 (first entry)
XX
XX Att site nucleotide sequence attR1.
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; att; ds.
XX
XX Synthetic.
OS
XX WO200295055-A2.
PN
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US15947.
XX
XX 21-MAY-2001; 2001US-291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule
PT for selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid -
XX
XX Disclosure; Fig 13A; 273pp; English.
XX
XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
CC represent att recombination site sequences used in the method of the
CC invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ
Query Match 100.0%; Score 25; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25
RESULT 10
ABT16628
ID APT16628 standard; DNA; 25 BP.
XX
XX APT16628;
AC APT16628;
XX
XX 03-APR-2003 (first entry)
XX
XX Artificial plant chromosome related oligo SEQ ID No 40.
XX
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX
XX Unidentified.
OS
XX WO200296923-A1.
PN
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US17451.
XX
XX 30-MAY-2001; 2001US-294687P.
PR
XX 04-JUN-2001; 2001US-296329P.
PR
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX (AGRI-) AGRISOMA INC.
XX
XX Perez C, Fabijanski SF, Perkins E;
XX
XX WPI; 2003-140436/13.
XX
XX Producing artificial chromosome by introducing a nucleic acid into
PT plant cell, selecting artificial chromosome that has one or more repeat
PT regions with equivalent amounts of euchromatic and heterochromatic
PT nucleic acids -
XX

```


AAF55743	
ID	AAF55743 standard; DNA; 25 BP.
XX	
XX	AAF55743;
XX	
XX	
DT	12-APR-2001 (first entry)
DE	Recombination site attrL
XX	
XX	Recombination site; cloning; att; ss.
OS	Unidentified.
XX	
PN	US6171861-B1.
PD	
XX	09-JAN-2001.
XX	
XX	12-JAN-1998; 98US-0005476.
PF	
PF	07-JUN-1996; 96US-0663002.
PR	07-JUN-1995; 95US-0486139.
XX	
XX	(LIFE-) LIFE TECHNOLOGIES INC.
PA	
XX	Hartley JL, Brasch MA;
PI	
XX	WPI; 2001-136877/14.
DR	
XX	
XX	In vitro cloning of nucleic acid involves mixing vectors comprising
PT	recombination sites and/or nucleic acid, incubating mixture to produce
PT	chimeric molecule, contacting hosts with mixture and selecting host -
PT	
XX	Claim 25; Column 46; 73pp; English.
XX	
XX	The present invention relates to a method for in vitro cloning of a
CC	nucleic acid of interest. The method involves mixing in vitro two vectors
CC	each comprising at least one recombination site and the nucleic acid of
CC	interest; incubating the mixture in the presence of at least one
CC	recombination protein to result in recombination of the recombination
CC	sites, leading to production of a chimeric nucleic acid molecule
CC	comprising the nucleic acid of interest; contacting hosts with the
CC	mixture; and selecting for a host comprising the chimeric nucleic acid
CC	molecule, and selecting against a host comprising the vectors comprising
CC	the second vector, to clone the nucleic acid. The present sequence is a
CC	recombination site, which may be used in the method of the present
CC	invention.
XX	
XX	Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
SQ	
Query Match	100.0%; Score 25; DB 22; Length 25;
Best Local Similarity	100.0%; Pred. No. 0.32;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GTTCAGCTTTTGTACAAACTTGT 25
DB	1 GTTCAGCTTTTGTACAAACTTGT 25
RESULT 6	
AAC87874	
ID	AAC87874 standard; DNA; 25 BP.
XX	
XX	AAC87874;
XX	
DT	02-MAR-2001 (first entry)
XX	
XX	Escherichia coli core region recombinant site attrL SEQ ID NO:9.
DE	
XX	Core region; recombination site; cloning; chimeric DNA;
XX	characteristic; mutation; att site; lox site; ss.
KW	
XX	Escherichia coli.
OS	
XX	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:05:38 ; Search time 111.5 Seconds
(without alignments)

605.255 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaactgt 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_19Jun03.*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	18	AA148218
2	25	100.0	25	20	AA178943
3	25	100.0	25	22	AA14437
4	25	100.0	25	22	AA14437
5	25	100.0	25	22	AA14437
6	25	100.0	25	22	AA14437
7	25	100.0	25	24	AA14437
8	25	100.0	25	25	AA14437

9	25	100.0	25	25	ABZ58734	Att site nucleotid
10	25	100.0	25	25	ABT16628	Artificial plant c
11	25	100.0	35	22	AAH19591	Plasmid pBZC7201 c
12	25	100.0	35	24	ABL58593	Oligonucleotide MO
13	25	100.0	43	21	AAC55545	att site PCR prime
14	25	100.0	43	22	AA506217	PCR primer attr1 u
15	25	100.0	82	21	AAC55503	Destination vector
16	25	100.0	87	21	AAC55517	Destination vector
17	25	100.0	95	21	AAC55497	Destination vector
18	25	100.0	102	21	AAC55458	GST expression cas
19	25	100.0	102	21	AAC55500	Destination vector
20	25	100.0	102	21	AAC55505	Destination vector
21	25	100.0	102	21	AAC55508	Destination vector
22	25	100.0	102	21	AAC55511	Destination vector
23	25	100.0	120	21	AAC55453	Trc expression cas
24	25	100.0	125	21	AAC55384	Recombination site
25	25	100.0	153	21	AAC55485	Destination vector
26	25	100.0	153	21	AAC55488	Destination vector
27	25	100.0	204	21	AAC55465	Destination vector
28	25	100.0	204	21	AAC55470	Destination vector
29	25	100.0	204	21	AAC55476	Destination vector
30	25	100.0	255	21	AAC55460	His6-Trx expressio
31	25	100.0	255	21	AAC55478	Destination vector
32	25	100.0	306	21	AAC55468	Destination vector
33	25	100.0	306	21	AAC55514	Destination vector
34	25	100.0	420	21	AAC55492	Destination vector
35	25	100.0	1846	24	AA144626	Gateway transfer c
36	25	100.0	4554	21	AAC55541	attr reading frame
37	25	100.0	5148	24	AA127063	Plasmid pGN39 DNA.
38	25	100.0	5848	21	AAC55481	Destination vector
39	25	100.0	5957	21	AAC55464	Destination vector
40	25	100.0	5957	21	AAC55467	Destination vector
41	25	100.0	6025	21	AAC55469	Destination vector
42	25	100.0	6264	21	AAC55507	Destination vector
43	25	100.0	6354	21	AAC55491	Destination vector
44	25	100.0	6422	21	AAC55483	Destination vector
45	25	100.0	6464	21	AAC55454	Destination vector

ALIGNMENTS

RESULT 1

AA148218

ID AA148218 standard; DNA; 25 BP.

XX

AC AA148218;

XX

DT 20-OCT-1997 (first entry)

XX

DE attR1 core region.

XX

KW att recombination site; core region; mutation; enhance; recombination;

KW vector; subcloning; regulation; exchange; ss.

XX

OS Synthetic.

XX

FN WO9640724-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US10082.

XX

PR 07-JUN-1995; 95US-0486139.

XX

PA (LIFE-) LIFE TECHNOLOGIES INC.

XX

PI Brasch MA, Hartley JL;

XX

DR WPI; 1997-065168/06.

XX

PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
using recombinant proteins and engineered recombination sites in

```

TITLE      Recombinational cloning using engineered recombination sites
JOURNAL    Patent: US 6171861-A 16 09-JAN-2001;
FEATURES
  source    1. .25
            Location/Qualifiers
BASE COUNT  5 a      4 c      6 g      10 t
ORIGIN
Query Match      83.2%; Score 20.8; DB 6; Length 25;
Best Local Similarity 91.7%; Pred.No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTTCAGCTTTTGTACAAACTTG 24
        |||||
Db      1 GTTCAGCTTTTGTACAAAGTTG 24
        |||||

Search completed: November 6, 2003, 23:06:41
Job time : 603 secs

```

ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 145569)
 Giselle,H.
 Direct Submission
 Submitted (12-DEC-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk
 Clone requests: clonerequest@sanger.ac.uk
 On Dec 16, 2002 this sequence version replaced gi.24940082.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: zface@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest, except on the rare
 occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names
 beginning 'dr' were identified by the Recon repeat discovery system
 (Zhifeng Bao and Sean Eddy, submitted), and those beginning 'drr'
 were identified by Rick Waterman (Stephen Johnson lab, WashU). For
 further information see http://www/Projects/D_rerio/fishmask.shtml
 CH211-237E12 is from a CHORI-211 BAC library
 VECTOR: pTARBAC2.1.

FEATURES
 source
 1..145569
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="CH211-237E12"
 /clone_lib="CHORI-211"
 BASE COUNT 48166 a 26034 c 25755 g 45614 t
 ORIGIN

Query Match 87.2%; Score 21.8; DB 5; Length 145569;
 Best Local Similarity 92.0%; Pred. No. 32;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTGT 25
 |||||
 Db 43543 GTTCTGCTTTTGTGACAAACTTAT 43567

RESULT 38
 BD131369
 LOCUS
 DEFINITION Recombinational cloning using nucleic acids having recombination
 sites.
 ACCESSION BD131369
 VERSION BD131369.1 GI:23226314
 KEYWORDS JP 2002500861-A/43.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS

AUTHORS
 TITLE
 JOURNAL

COMMENT

Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
 Recombinational cloning using nucleic acids having recombination
 Patent: JP 2002500861-A 43 15-JAN-2002;
 LIFE TECHNOLOGIES INC
 OS Unknown
 PN JP 2002500861-A/43
 PD 15-JAN-2002
 PF 26-OCT-1998 JP 2000518069
 PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PT
 JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
 C12N15/09, C12Q1/68, C12N15/00
 CC Description of Unknown Organism: recombination products PH
 Key Location/Qualifiers
 FT source 1..25
 /organism="Unknown".

FEATURES
 source
 1..25
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

BASE COUNT 4 a 3 c 5 g 10 t 3 others
 ORIGIN

Query Match 84.8%; Score 21.2; DB 6; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 20; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTG 24
 |||||
 Db 1 GTTCAGCTTTTGTGACAAACTTG 24

RESULT 39
 AR124531
 LOCUS
 DEFINITION Sequence 11 from patent US 6171861.
 ACCESSION AR124531
 VERSION AR124531.1 GI:14109892
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L. and Brasch,M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..25
 /organism="unknown"

BASE COUNT 5 a 4 c 6 g 10 t
 ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 25;
 Best Local Similarity 91.7%; Pred. No. 4.3e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAAACTTG 24
 |||||
 Db 1 GTTCAGCTTTTGTGACAAACTTG 24

RESULT 40
 AR124536
 LOCUS
 DEFINITION Sequence 16 from patent US 6171861.
 ACCESSION AR124536
 VERSION AR124536.1 GI:14109897
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley,J.L. and Brasch,M.A.

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 33
AX525413/c
LOCUS AX525413 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 11 from Patent WO02066622.
ACCESSION AX525413
VERSION AX525413.1 GI:25170299
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tsutsumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 11 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
Location/Qualifiers
1..51
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="051200j1"

BASE COUNT 15 a 10 c 17 g 9 t
ORIGIN

Query Match 87.2%; Score 21.8; DB 6; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 34
AX525421/c
LOCUS AX525421 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 19 from Patent WO02066622.
ACCESSION AX525421
VERSION AX525421.1 GI:25170307
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tsutsumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 19 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
Location/Qualifiers
1..51
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="051200j9"

BASE COUNT 16 a 10 c 15 g 10 t
ORIGIN

Query Match 87.2%; Score 21.8; DB 6; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 35

AX525429/c
LOCUS AX525429 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 27 from Patent WO02066622.
ACCESSION AX525429
VERSION AX525429.1 GI:25170315
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tsutsumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 27 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
Location/Qualifiers
1..51
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="051200j17"

BASE COUNT 14 a 12 c 16 g 9 t
ORIGIN

Query Match 87.2%; Score 21.8; DB 6; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 36
AX525456/c
LOCUS AX525456 51 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 54 from Patent WO02066622.
ACCESSION AX525456
VERSION AX525456.1 GI:25170342
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Tsutsumi,N., Vind,J. and Patkar,S.A.
TITLE Lipolytic enzyme genes
JOURNAL Patent: WO 02066622-A 54 29-AUG-2002;
Novozymes A/S (DK)

FEATURES
Location/Qualifiers
1..51
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="080201P1"

BASE COUNT 18 a 10 c 13 g 10 t
ORIGIN

Query Match 87.2%; Score 21.8; DB 6; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 29 GTCTGCTTTTGTACAAACTTGT 5

RESULT 37
AL935194
LOCUS AL935194 145569 bp DNA linear VRT 13-DEC-2002
DEFINITION Zebrafish DNA sequence from clone CH211-237E12, complete sequence.
ACCESSION AL935194
VERSION AL935194.4 GI:26985414
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)

silencing in plants
 Plant J. 27 (5), 581-590 (2001)
 JOURNAL MEDLINE 21461301
 PUBMED 11576441
 REFERENCE 2 (bases 1 to 18691)
 AUTHORS Waterhouse, P.M.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
 C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
 FEATURES location/Qualifiers
 source
 1..18691
 /organism="Cloning vector pHELLSGATE"
 /mol_type="genomic DNA"
 /db_xref="taxon:167049"
 /lab_host="Escherichia coli"
 /focus="pHELLSGATE is a derivative of cloning vector PART27"
 1..264
 /organism="Escherichia coli K12"
 /mol_type="genomic DNA"
 /strain="K12"
 /db_xref="taxon:83333"
 265..448
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 449..1442
 /organism="Escherichia coli"
 /mol_type="genomic DNA"
 /db_xref="taxon:562"
 1443..7792
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 7793..9388
 /organism="Escherichia coli"
 /mol_type="genomic DNA"
 /db_xref="taxon:562"
 9389..11673
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 11674..13019
 /organism="Cauliflower mosaic virus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10641"
 14660..16258
 /organism="Flaveria trinervia"
 /mol_type="genomic DNA"
 /db_xref="taxon:4227"
 17922..18691
 /organism="Agrobacterium tumefaciens"
 /mol_type="genomic DNA"
 /db_xref="taxon:358"
 284..447
 /function="NOS promoter"
 448..1269
 /gene="nptII"
 448..1269
 /gene="nptII"
 /notes="neomycin phosphotransferase II (nptII)"
 /codon_start=1
 /product="kanomycin resistance protein"
 /protein_id="CAC86252.1"
 /db_xref="GI:15982219"
 /db_xref="REMBL:CAC86252"
 /translation="MAITLSATSLPISARIRAGSPAAVVERFLGYDWAQQTIGCSDDAA
 VFLRSAGQRPVLFVKTDLSGALNEQEARLSWLATTPGCAAVLDVVTAGRWLL
 LGEVPCQDLSHLAPAEKVSIMADARLITLDPATCPDHOAKHRIERATRMEAG
 LVDQDLDEHQGLAPAEFLFARKMPGEGDLVTHGDACLPNTMVENGRSGFIDC
 GRUGVADRYQDIALATRDIAELGGEWADRFLVLYGIAAPDSQRIAFYLLDEFF"

terminator 1443..2148
 /note="NOS terminator"
 repeat_region 2149..2706
 /note="left border"
 repeat_region 7793..9388
 /transposon="Tn7"
 8600..9388
 /gene="spec"
 8600..9388
 /gene="spec"
 /codon_start=1
 /transl_table=11
 /product="spectinomycin resistance protein"
 /protein_id="CAC86253.1"
 /db_xref="GI:15982220"
 /db_xref="REMBL:CAC86253"
 /translation="MRBAVIAEVSTQSEVVGVLIERHLEPTLLAVHLYGSAVDGGLKP
 HSDIDLLVTVRLEDTTRRALINDLETASGSEILRAVEVTIVHDDIIPWRYP
 AKRELQGEWQRNDILAGIFEPATIDIDILTKAREHVALVGPAAEELDFVPEQ
 DLFEALNETLTLWNSPPDWAGDERNVLTLSIWSAVTGTKIAPKDVAAADWAMERLPA
 QYQPVLEARQAYLGQEDRLASRADQLSEFVHYVKBITTKVVGK"
 10706..11324
 /note="right border"
 11674..13019
 /function="35S promoter"
 14660..16258
 /gene="pdk"
 14660..16258
 /gene="pdk"
 /note="Pyruvate orthophosphate dikinase (pdk)"
 /number=2
 17922..18687
 /note="octopine esynthase (ocs) terminator"
 BASE COUNT 4837 a 4621 c 4607 g 4626 t
 ORIGIN
 Query Match 89.6%; Score 22.4; DB 12; Length 18691;
 Best Local Similarity 95.8%; Pred. No. 26;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTCAGCTTTTGTGACAACTTG 24
 |||||
 Db 13146 GTTCAGCTTTTGTGACAAAGTTG 13123
 RESULT 32
 AX269136
 LOCUS AX269136 25 bp DNA linear PAT 29-OCT-2001
 DEFINITION Sequence 7 from Patent WO0174861.
 ACCESSION AX269136
 VERSION AX269136.1 GI:16542056
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Vile, R.G., Harrington, K., Murphy, S. and Bateman, A.
 TITLE Compositions and methods for tissue specific gene regulation
 therapy
 JOURNAL Patent: WO 0174861-A 7 11-OCT-2001;
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
 FEATURES location/Qualifiers
 source
 1..25
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Synthetically generated vector sequence"
 BASE COUNT 5 a 5 c 4 g 10 t 1 others
 ORIGIN
 Query Match 87.2%; Score 21.8; DB 6; Length 25;
 Best Local Similarity 92.0%; Pred. No. 1.6e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

KEYWORDS kanomycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.

SOURCE Cloning vector pHELLSGATE

ORGANISM Cloning vector pHELLSGATE

REFERENCE artificial sequences; vectors.

AUTHORS Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.

TITLE Construct design for efficient, effective and high-throughput gene silencing in plants

JOURNAL Plant J. 27 (6), 581-590 (2001)

MEDLINE 21461301

PUBMED 11576441

REFERENCE 2 (bases 1 to 18691)

AUTHORS Waterhouse, P.M.

TITLE Direct Submission

JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

FEATURES Location/Qualifiers

1..18691

/organism="Cloning vector pHELLSGATE"

/mol_type="genomic DNA"

/db_xref="taxon:167049"

/lab_host="Escherichia coli"

/focus

/note="pHELLSGATE is a derivative of cloning vector pART27"

1..264

/organism="Escherichia coli K12"

/mol_type="genomic DNA"

/strain="K12"

/db_xref="taxon:83333"

265..448

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

449..1442

/organism="Escherichia coli"

/mol_type="genomic DNA"

/db_xref="taxon:562"

1443..7792

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

7793..9388

/organism="Escherichia coli"

/mol_type="genomic DNA"

/db_xref="taxon:562"

9389..11673

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

11674..13019

/organism="Cauliflower mosaic virus"

/mol_type="genomic DNA"

/db_xref="taxon:10641"

14660..16258

/organism="Flavaria trinervia"

/mol_type="genomic DNA"

/db_xref="taxon:4227"

17922..18691

/organism="Agrobacterium tumefaciens"

/mol_type="genomic DNA"

/db_xref="taxon:358"

264..447

/function="NOS promoter"

448..1269

/gene="nptII"

448..1269

/gene="nptII"

CDS Construct design for efficient, effective and high-throughput gene

/codon_start=1

/transl_table=11

/product="kanomycin resistance protein"

/protein_id="CAC86252.1"

/db_xref="GI:15982219"

/db_xref="REMTREMBL:CAC86252"

/translation="MAITLSATSLPISARIRAGSPAAWVERLFGYDMAQQTIGCSDAALVERLSAQRPVLVFKTDLGSLNLEQDEARLSWLAATGVCAAVLDTVTAGRDWILLGVEPGDQLLSHLAPAEKVSIMADAMERLHTLPATCFDHOAKHRTERTARMEAGLVQDDDLDEHQGLAPAEFLPARLXARMPDGEDLVVTHGDACLPLIMVENGHESGFLDCGRLGVDARYQDIALATRDIAEELGEGWADRFLVLYGIAAPDSQRIAFRLLDFFF"

1443..2148

terminator

/note="NOS terminator"

2149..2706

repeat_region

/note="left border"

7793..9388

repeat_region

/transposon="Tn7"

9600..9388

gene

/gene="spec"

9600..9388

CDS

/gene="spec"

/codon_start=1

/transl_table=11

/product="spectinomycin resistance protein"

/protein_id="CAC86253.1"

/db_xref="GI:15982220"

/db_xref="REMTREMBL:CAC86253"

/translation="MREAVIAVSTQLSEVWGVIERHLEPTLLAVHLYGSADVGGGLKP HSDIDLVTVVRDLDETTRRLINLLDLSASPGESEILRAVEVTIVVHDDILPKRYP AKRELQGEWQRNDLAGIFEPATIDIDLILLTKAREHSVALVGPAEELDFPVEQ DLFEALNETLTLWNSPPDWAGDNRNVLTLSRIWYSAVTGKIAKPDVAADWAWERLPA QYQVILBARQAYLGQEDRLASRADQLEEFVHVKEITKVYVK"

10706..11324

repeat_region

/note="right border"

11674..13019

promoter

/function="35S promoter"

14660..16258

gene

/gene="pdk"

14660..16258

intron

/gene="pdk"

/note="pyruvate orthophosphate dikinase (pdk)"

/number=2

17922..18697

terminator

/note="octopine esynthase (ocs) terminator"

BASE COUNT 4837 a 4621 c 4607 g 4626 t

ORIGIN

Query Match 89.6%; Score 22.4; DB 12; Length 18691;

Best Local Similarity 95.8%; Pred. No. 26;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTGACAACTTG 24

|||||

Db 17792 GTTCAGCTTTTGTGACAACTTG 17815

RESULT 31

CVE311874/c

LOCUS CVE311874 18691 bp DNA circular SYN 09-JUL-2002

DEFINITION Cloning vector pHELLSGATE.

ACCESSION AJ311874

VERSION AJ311874.1 GI:15982218

KEYWORDS kanomycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.

SOURCE Cloning vector pHELLSGATE

ORGANISM Cloning vector pHELLSGATE

REFERENCE 1

AUTHORS artificial sequences; vectors.

Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.

TITLE Construct design for efficient, effective and high-throughput gene

Accession	AF30825	GI:23343422			
Version	AX498625.1				
Keywords					
Source	unidentified				
Organism	unidentified				
LOCUS	CVE311874	18691 bp	DNA	circular	SYN 09-JUL-2002
DEFINITION	Cloning vector				
ACCESSION	AJ311874				
VERSION	AJ311874.1	GI:15982218			

```

RESULT 22
AX498620      AX498620      25 bp      DNA      linear      PAT 26-SEP-2002
LOCUS
DEFINITION    Sequence 10 from Patent EP1229113.
ACCESSION     AX498620
VERSION       AX498620.1  GI:23343417
KEYWORDS
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       INVITROGEN CORPORATION (US)
FEATURES
source        1. .25
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT    5 a 5 c 4 g 11 t
ORIGIN

Query Match   93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 23
BD131336
LOCUS
DEFINITION    Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION     BD131336
VERSION       BD131336.1  GI:23226281
KEYWORDS      JP 2002500861-A/10.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 25)
AUTHORS       Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE         Recombinational cloning using nucleic acids having recombination
LIFE TECHNOLOGIES INC
COMMENT       OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
KEY
FT source      1. .25
              Location/Qualifiers
              /organism="Unknown"
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT    5 a 5 c 4 g 11 t
ORIGIN

Query Match   93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 24
BD131336
LOCUS
DEFINITION    Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION     BD131336
VERSION       BD131336.1  GI:23226313
KEYWORDS      JP 2002500861-A/42.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 25)
AUTHORS       Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE         Recombinational cloning using nucleic acids having recombination
JOURNAL       LIFE TECHNOLOGIES INC
COMMENT       OS Unknown
PN JP 2002500861-A/42
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
KEY
FT source      1. .25
              Location/Qualifiers
              /organism="Unknown"
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT    4 a 3 c 3 g 9 t 6 others
ORIGIN

Query Match   90.4%; Score 22.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 74;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 25
AR124535
LOCUS
DEFINITION    Sequence 15 from patent US 6171861.
ACCESSION     AR124535
VERSION       AR124535.1  GI:14109896
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 25)
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       Patent: US 6171861-A 15 09-JAN-2001;
FEATURES
source        1. .25
              Location/Qualifiers
              /organism="unknown"
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT    5 a 3 c 6 g 11 t
ORIGIN

Query Match   89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 24

```

```

Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 24
BD131368
LOCUS
DEFINITION    Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION     BD131368
VERSION       BD131368.1  GI:23226313
KEYWORDS      JP 2002500861-A/42.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 25)
AUTHORS       Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE         Recombinational cloning using nucleic acids having recombination
JOURNAL       LIFE TECHNOLOGIES INC
COMMENT       OS Unknown
PN JP 2002500861-A/42
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
KEY
FT source      1. .25
              Location/Qualifiers
              /organism="Unknown"
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT    4 a 3 c 3 g 9 t 6 others
ORIGIN

Query Match   90.4%; Score 22.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 74;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 25
AR124535
LOCUS
DEFINITION    Sequence 15 from patent US 6171861.
ACCESSION     AR124535
VERSION       AR124535.1  GI:14109896
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 25)
AUTHORS       Hartley,J.L. and Brasch,M.A.
TITLE         Recombinational cloning using engineered recombination sites
JOURNAL       Patent: US 6171861-A 15 09-JAN-2001;
FEATURES
source        1. .25
              Location/Qualifiers
              /organism="unknown"
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT    5 a 3 c 6 g 11 t
ORIGIN

Query Match   89.6%; Score 22.4; DB 6; Length 25;
Best Local Similarity 95.8%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 24

```

```

Construction of Neurospora crassa Histidine-3 (his-3)-Gene
Replacement Plasmids
Unpublished
REFERENCE 2 (bases 1 to 13990)
AUTHORS Haag,J.R., Lee,D.W. and Aramayo,R.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Biology, Texas A&M University, BSBW #415,
College Station, TX 77843-3258, USA
FEATURES
source
1..13990
Location/Qualifiers
/organism="his-3 integration vector pUHAM007"
/mol_type="genomic DNA"
/specific_host="Neurospora crassa"
/db_xref="taxon:211505"
1..3173
/note="pCEM132f(+)"
misc_feature
3174..8368
/note="his-3 left flank; his-3 target integration site"
misc_feature
8430..8554
/note="attR1; Gateway; Bacteriophage Lambda recombination
site"
CDS
8804..9463
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="AA076304.1"
/db_xref="GI:25988998"
/translation="MEKKTGYTVDISQWHRKEHFEAFQSVAACTYNCTVOLDITAF
LKTVMKHKFPAPTHILARLMAHPERMAKDELVLWDSVHPCVTVPEHQPETF
SSLSSEYHDDPQFLHYSQDVACYGELAYFPKGFENWFFVSANPVVFTSFLNV
AAMDNFFAFVFTMGKYYTGQDKVLMPLAIQVHHAVCDFGHVGRMLNELQQYCDWQGG
A"
8905..10110
/note="ccdB"
/codon_start=1
/product="gyrase target toxin"
/protein_id="AA076305.1"
/db_xref="GI:25988999"
/translation="MDFKVTYTKRESRYELFVDVSDIIDTPGRRMVPLASARLLSD
KVSRELYPVVHIGDESRWMTTDMASVPVSGEEVADLSHRENDIKNAINLMFWGI"
10151..10275
/note="attR2; Gateway; Bacteriophage Lambda recombination
site"
misc_feature
10419..13990
/note="his-3 right flank; his-3 target integration site"
BASE COUNT 3385 a 3549 c 3559 g 3497 t
ORIGIN
Query Match 100.0%; Score 25; DB 12; Length 13990;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 8454 GTTCAGCTTTTGTACAAACTTGT 8430

RESULT 19
LOCUS AR124530 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6171861.
ACCESSION AR124530
VERSION AR124530.1 GI:14109891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 10 09-JAN-2001;
FEATURES
source
1..25
Location/Qualifiers
/organism="unknown"

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 20
LOCUS AR163181 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 10 from patent US 6270969.
ACCESSION AR163181
VERSION AR163181.1 GI:16233690
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 10 07-AUG-2001;
FEATURES
source
1..25
Location/Qualifiers
/organism="unknown"

BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 21
LOCUS AX491649 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 10 from Patent EP1227147.
ACCESSION AX491649
VERSION AX491649.1 GI:22324157
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 10 31-JUL-2002;
FEATURES
source
1..25
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 5 a 5 c 4 g 11 t
ORIGIN
Query Match 93.6%; Score 23.4; DB 6; Length 25;
Best Local Similarity 96.0%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

```

Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 4760 GTTCAGCTTTTGTACAAACTTGT 4784

RESULT 15
AX196825/c
LOCUS AX196825 12677 bp DNA circular SYN 26-FEB-2003
DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AX196825
VERSION AX196825.1 GI:28565731
KEYWORDS piggyBac transformation vector pB-UGIR w+
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.

REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 12677)
AUTHORS Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC 27709, USA

FEATURES
source
1..12677
/organism="piggyBac transformation vector pB-UGIR w+"
/mol_type="genomic DNA"
/db_xref="taxon:221642"
complement(11..>620)
/transposon="piggyBac transposable element"
632..998
/note="5x UAS hsp70 TATA signal"
1003..2713
/note="Gateway recombination cassette A; attR1 Cmr codb
attR2"
2726..3040
/note="RpS5"
/number=3
complement(3076..4788)
/note="Gateway recombination cassette B; attR1 Cmr codb
attR2"
4789..5246
/note="SV40"
5247..9369
/gene="w"
/note="mini-white; derived from Drosophila"
complement(<9370..9819)
/transposon="piggyBac transposable element"

BASE COUNT 3423 a 2924 c 2833 g 3497 t
ORIGIN

Query Match 100.0%; Score 25; DB 12; Length 12677;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 1030 GTTCAGCTTTTGTACAAACTTGT 1006

RESULT 16
AX590202
LOCUS AX590202 12789 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02083888.
ACCESSION AX590202
VERSION AX590202.1 GI:27901286
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Goossens, A. and Inz, D.
TITLE The use of genes encoding membrane transporter pumps to stimulate the production of secondary metabolites in biological cells
JOURNAL Patent: WO 02083888-A 9 24-OCT-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)

FEATURES
source
1..12789
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="vector pK7WG2D"

BASE COUNT 3050 a 3326 c 3397 g 3015 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 12789;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 3701 GTTCAGCTTTTGTACAAACTTGT 3725

RESULT 17
AX356862
LOCUS AX356862 13274 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 20 from Patent WO0206490.
ACCESSION AX356862
VERSION AX356862.1 GI:18674110
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Dudler, R., Schaffrath, U. and Lawton, K.A.
TITLE Lipoxigenase genes, promoters, transit peptides and proteins thereof
JOURNAL Patent: WO 0206490-A 20 24-JAN-2002;
Syngenta Location/Qualifiers

FEATURES
source
1..13274
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 3343 a 3271 c 3178 g 3482 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 13274;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAAACTTGT 25
|||||
Db 4026 GTTCAGCTTTTGTACAAACTTGT 4050

RESULT 18
AF541939/c
LOCUS AF541939 13990 bp DNA linear SYN 01-DEC-2002
DEFINITION His-3 integration vector pJHAM007, complete sequence.
ACCESSION AF541939
VERSION AF541939.1 GI:25988997
KEYWORDS his-3 integration vector pJHAM007
SOURCE his-3 integration vector pJHAM007
ORGANISM his-3 integration vector pJHAM007
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 13990)
AUTHORS Haag, J.R., Lee, D.W. and Aramayo, R.
TITLE Description of a GATEWAY Destination Vector For High-Throughput

```

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
    source
        1..11005
        /organism="piggyBac transformation vector pB-UGateway w+"
        /mol_type="genomic DNA"
        /db_xref="taxon:221641"
        complement(11..>620)
    repeat_region
        /transposon="piggyBac transposable element"
    TATA_signal
        643..999
        /note="5x UAS hsp70 TATA signal"
    misc_feature
        1003..2713
        /note="Gateway recombination cassette A; attR1 CmR ccdB
        attR2"
    intron
        2726..3040
        /note="RpS5"
        /number=3
    polyA_signal
        3072..3573
        /note="SV40"
    gene
        3574..7697
        /gene="w"
    repeat_region
        /note="mini-white; derived from Drosophila"
        complement(<7698..8147)
    /transposon="piggyBac transposable element"
    BASE COUNT 2952 a 2528 c 2491 g 3034 t
    ORIGIN
        Query Match 100.0%; Score 25; DB 12; Length 11005;
        Best Local Similarity 100.0%; Pred. No. 2.3;
        Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
    |||||||
Db 3089 GTTCAGCTTTTGTACAACTTGT 3113

RESULT 13
AY196824/c AY196824 11005 bp DNA circular SYN 26-FEB-2003
LOCUS PiggyBac transformation vector pB-UGateway w+, complete sequence.
DEFINITION
ACCESSION AY196824
VERSION AY196824.1 GI:28565716
KEYWORDS
SOURCE piggyBac transformation vector pB-UGateway w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11005)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
    source
        1..11005
        /organism="piggyBac transformation vector pB-UGateway w+"
        /mol_type="genomic DNA"
        /db_xref="taxon:221641"
        complement(11..>620)
    repeat_region
        /transposon="piggyBac transposable element"
        643..999
    TATA_signal
        1003..2713
        /note="5x UAS hsp70 TATA signal"
    misc_feature
        1003..2713
        /note="Gateway recombination cassette A; attR1 CmR ccdB
        attR2"

```

```

attR2"
2726..3040
/number=3
polyA_signal
3072..3573
/note="SV40"
3574..7697
/gene="w"
repeat_region
/note="mini-white; derived from Drosophila"
complement(<7698..8147)
/transposon="piggyBac transposable element"
BASE COUNT 2952 a 2528 c 2491 g 3034 t
ORIGIN
    Query Match 100.0%; Score 25; DB 12; Length 11005;
    Best Local Similarity 100.0%; Pred. No. 2.3;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
    |||||||
Db 1030 GTTCAGCTTTTGTACAACTTGT 1006

RESULT 14
AY196825 AY196825 12677 bp DNA circular SYN 26-FEB-2003
LOCUS PiggyBac transformation vector pB-UGIR w+, complete sequence.
DEFINITION
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
KEYWORDS
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
    source
        1..12677
        /organism="piggyBac transformation vector pB-UGIR w+"
        /mol_type="genomic DNA"
        /db_xref="taxon:221642"
        complement(11..>820)
    repeat_region
        /transposon="piggyBac transposable element"
        632..998
    TATA_signal
        /note="5x UAS hsp70 TATA signal"
        1003..2713
    misc_feature
        /note="Gateway recombination cassette A; attR1 CmR ccdB
        attR2"
        2726..3040
        /note="RpS5"
        /number=3
    misc_feature
        complement(3076..4788)
        /note="Gateway recombination cassette B; attR1 CmR ccdB
        attR2"
        4789..5246
        /note="SV40"
        5247..9369
        /gene="w"
        /note="mini-white; derived from Drosophila"
        complement(<9370..9819)
    repeat_region
        /transposon="piggyBac transposable element"
        3423 a 2924 c 2833 g 3497 t
    BASE COUNT 3423 a 2924 c 2833 g 3497 t
    ORIGIN
        Query Match 100.0%; Score 25; DB 12; Length 12677;

```

```

misc_feature      A"
                  complement(3657..3783)
/notes="attr1 of Gateway conversion cassette frame A"
BASE COUNT      2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match      100.0%; Score 25; DB 12; Length 9019;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
Db 3756 GTTCAGCTTTTGTACAAACTTGT 3780

RESULT 11
AF408413/c
LOCUS             AF408413             9019 bp    DNA      circular SYN 25-JUN-2002
DEFINITION        Binary vector pJawohl8-RNAi, complete sequence.
ACCESSION         AF408413
VERSION           AF408413.1 GI:21552736
KEYWORDS
SOURCE            Binary vector pJawohl8-RNAi
ORGANISM          Binary vector pJawohl8-RNAi
                  artificial sequences; vectors.
REFERENCE         1 (bases 1 to 9019)
AUTHORS           Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE             pJawohl8-RNAi a binary vector for gene silencing in plants
JOURNAL           Unpublished
REFERENCE         2 (bases 1 to 9019)
AUTHORS           Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
TITLE             Direct Submission
JOURNAL           Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
                  f. Zuechtungsforshung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
                  Germany
FEATURES           Location/Qualifiers
source             1..9019
                  /organism="Binary vector pJawohl8-RNAi"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:188084"
                  /focus
note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803..9019
/organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:176105"
26..1733
/notes="sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, CmR gene and ccdB
gene"
26..152
/notes="attr1 of Gateway conversion cassette frame A"
262..921
/gene="CmR"
262..921
/gene="CmR"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="CmR"
/protein_id="AAM62300.1"
/db_xref="GI:21552737"
/translation="MEKKTGYTTVDISQWHRKEHFEAFQSVQACTYNOTVQDITAF
LKTVMKNKHFYPAFHILARLMAHPEFVAMKDGELVINDSVHPCYTFVHEQTEF
SSLWSEYHDDFRQFLHIYSQVACYGENLAYFPKGFIENMFVSNPWSFTSFDLNV
ANMNDFFAPVFTMGKIYTGQDKVLMPLAIQVHHAUCDGFHVRMLNELQQYCDWEQGG
A"
1263..1568
/gene="ccdB"
1263..1568
/gene="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison

```

```

of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62301.1"
/db_xref="GI:21552738"
/translation="MOKVYTYKRSRYRLFVDVQSDIIDTPGRRWVIPLASARLLSD
KVSRELYPVVHIGDESRWMTDMASVPVSVIGEEVADLSHRENDIKNAINLFWGIGI"
1610..1736
/notes="attr2 of Gateway conversion cassette frame A"
1762..2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
/notes="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, CmR gene and
ccdB gene"
complement(2073..2199)
/notes="attr2 of Gateway conversion cassette frame A"
complement(2241..2546)
/gene="ccdB"
complement(2241..2546)
/gene="ccdB"
/notes="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62303.1"
/db_xref="GI:21552740"
/translation="MOKVYTYKRSRYRLFVDVQSDIIDTPGRRWVIPLASARLLSD
KVSRELYPVVHIGDESRWMTDMASVPVSVIGEEVADLSHRENDIKNAINLFWGIGI"
complement(2888..3547)
/gene="CmR"
complement(2888..3547)
/gene="CmR"
/function="confers resistance to antibiotic
chloramphenicol"
/codon_start=1
/product="CmR"
/protein_id="AAM62302.1"
/db_xref="GI:21552739"
/translation="MEKKTGYTTVDISQWHRKEHFEAFQSVQACTYNOTVQDITAF
LKTVMKNKHFYPAFHILARLMAHPEFVAMKDGELVINDSVHPCYTFVHEQTEF
SSWSEYHDDFRQFLHIYSQVACYGENLAYFPKGFIENMFVSNPWSFTSFDLNV
ANMNDFFAPVFTMGKIYTGQDKVLMPLAIQVHHAUCDGFHVRMLNELQQYCDWEQGG
A"
complement(3657..3783)
/notes="attr1 of Gateway conversion cassette frame A"
BASE COUNT      2337 a 2150 c 2185 g 2347 t
ORIGIN
Query Match      100.0%; Score 25; DB 12; Length 9019;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
    |||||
Db 53 GTTCAGCTTTTGTACAAACTTGT 29

RESULT 12
AF196824
LOCUS             AF196824             11005 bp    DNA      circular SYN 26-FEB-2003
DEFINITION        PiggyBac transformation vector pB-UGateway w+, complete sequence.
ACCESSION         AF196824
VERSION           AF196824.1 GI:28565716
KEYWORDS
SOURCE            PiggyBac transformation vector pB-UGateway w+
ORGANISM          piggyBac transformation vector pB-UGateway w+
                  artificial sequences; vectors.
REFERENCE         1 (bases 1 to 11005)
AUTHORS           Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE             A toolkit for transformation and mutagenesis in Drosophila using
                  piggyBac

```

ORIGIN

Query Match 100.0%; Score 25; DB 12; Length 4462;
 Best Local Similarity 100.0%; Pred. No. 2.7; 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 480 GTTCAGCTTTTGTACAACTTGT 456

RESULT 9

AX306327/c
 LOCUS AX306327 5148 bp DNA linear PAT 11-DEC-2001
 DEFINITION Sequence 10 from Patent WO0188121.
 ACCESSION AX306327

VERSION AX306327.1 GI:17645566

KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Plaetinck, G., Renard, J.P. and Bogaert, T.
 TITLE Vector constructs
 JOURNAL Patent: WO 0188121-A 10 22-NOV-2001;
 Devgen NV (BE)

FEATURES
 source
 1. 5148
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Plasmid pGN39"

BASE COUNT 1359 a 1199 c 1279 g 1311 t

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 5148;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
 |||||
 Db 171 GTTCAGCTTTTGTACAACTTGT 147

RESULT 10

AF408413
 LOCUS AF408413 9019 bp DNA circular SYN 25-JUN-2002
 DEFINITION Binary vector pJawohl8-RNAi, complete sequence.
 ACCESSION AF408413
 VERSION AF408413.1 GI:21552736

KEYWORDS
 SOURCE Binary vector pJawohl8-RNAi
 ORGANISM Binary vector pJawohl8-RNAi
 artificial sequences; vectors.

REFERENCE 1 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
 TITLE pJawohl8-RNAi a binary vector for gene silencing in plants
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 9019)
 AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
 TITLE Direct Submission
 JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
 f. zuechtungsforshung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
 Germany

FEATURES
 source
 1. 9019
 /organism="Binary vector pJawohl8-RNAi"
 /mol_type="genomic DNA"
 /db_xref="taxon:188084"
 /focus
 /note="binary plant gene silencing vector for one-step
 cloning of inverted sequences"

BASE COUNT 3803. .9019

/organism="Binary vector pJawohl8-RNAi"
 /mol_type="genomic DNA"
 /db_xref="taxon:176105"

repeat_region

26..1733
 /note="sense orientation of Gateway conversion cassette
 frame A containing attR1-R2 repeats, Cmr gene and ccdB
 gene"

misc_feature

26..152
 /note="attR1 of Gateway conversion cassette frame A"

gene

262..921
 /gene="Cmr"

CDS

262..921
 /gene="Cmr"

/function="confers resistance to antibiotic
 chloramphenicol"

/codon_start=1
 /product="Cmr"

/protein_id="AA62300.1"
 /db_xref="GI:21552737"

/translation="MEKITGYTVDISQHRKEHFAFQSVAACTYNQVLDITAF
 LKTVKKNKHFPAPFATHILARLNMAHPEFRMAKDGELVWDSVHPCTVFFHQETTF
 SSLWSEYHDDFRQFLHIYSQDVACYGENLAYPKGFENMFVSNPWPVSFSLNV
 ANMDFPAPVFTMGKYYTQGDVKVLMPLAIQVHHAUCDGFHVGRLNELQYCDWGG
 A"

gene

1263..1568
 /gene="ccdB"

CDS

1263..1568
 /gene="ccdB"

/note="encodes a cytotoxic protein that is a potent poison
 of DNA gyrase"

/codon_start=1

/product="CcdB"

/protein_id="AA62301.1"

/db_xref="GI:21552738"

/translation="MQFKYTYKRESRYLFDVQSDIIDTPGRRMVIPLASARLLSD
 KVSRELYPVVHIGDESWMRTDMASVPVSVIGEEVADLSHRENDIKNAIMFWGI"
 1610..1736

misc_feature

1762..2048
 /note="attR2 of Gateway conversion cassette frame A"

/note="contains intron 1 of Arabidopsis thaliana WRKY
 transcription factor 33"

complement(2073..3783)

/note="antisense orientation of Gateway conversion
 cassette frame A containing attR1-R2 repeats, Cmr gene and
 ccdB gene"

complement(2073..2199)

/note="attR2 of Gateway conversion cassette frame A"

complement(2241..2546)

/gene="ccdB"

complement(2241..2546)

/gene="ccdB"

/note="encodes a cytotoxic protein that is a potent poison
 of DNA gyrase"

/codon_start=1

/product="CcdB"

/protein_id="AA62303.1"

/db_xref="GI:21552740"

/translation="MQFKYTYKRESRYLFDVQSDIIDTPGRRMVIPLASARLLSD
 KVSRELYPVVHIGDESWMRTDMASVPVSVIGEEVADLSHRENDIKNAIMFWGI"
 complement(2888..3547)

/gene="Cmr"

complement(2888..3547)

/gene="Cmr"

/function="confers resistance to antibiotic
 chloramphenicol"

/codon_start=1

/product="Cmr"

/protein_id="AA62302.1"

/db_xref="GI:21552739"

/translation="MEKITGYTVDISQHRKEHFAFQSVAACTYNQVLDITAF
 LKTVKKNKHFPAPFATHILARLNMAHPEFRMAKDGELVWDSVHPCTVFFHQETTF
 SSLWSEYHDDFRQFLHIYSQDVACYGENLAYPKGFENMFVSNPWPVSFSLNV
 ANMDFPAPVFTMGKYYTQGDVKVLMPLAIQVHHAUCDGFHVGRLNELQYCDWGG
 A"

```

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 6
AX684690/c
LOCUS AX684690 35 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 9 from Patent WO0224865.
ACCESSION AX684690
VERSION AX684690.1 GI:29371240
KEYWORDS
SOURCE
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
TITLE Modulation of secondary metabolite production by zinc binuclear
cluster proteins
JOURNAL Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
FEATURES
source
1. .35
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
BASE COUNT 14 a 7 c 7 g 7 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 35 GTTCAGCTTTTGTACAAACTTGT 11

RESULT 7
AX703501/c
LOCUS AX703501 1846 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 63 from Patent WO02066653.
ACCESSION AX703501
VERSION AX703501.1 GI:29538461
KEYWORDS
SOURCE synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Li,M. and Liu,Y.C.
TITLE Prokaryotic libraries and uses
JOURNAL Patent: WO 02066653-A 63 29-AUG-2002;
Xencor (US)
FEATURES
source
1. .1846
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 527 a 381 c 434 g 504 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 1846;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAACTTGT 25
Db 25 GTTCAGCTTTTGTACAAACTTGT 1

RESULT 8
VF0551314/c
LOCUS VF0551314 4462 bp DNA circular SYN 27-MAR-2003
DEFINITION Transfection vector pBTdest.
ACCESSION VF0551314
VERSION VF0551314.1 GI:29335742
KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
acetyl transferase; control of cell death B protein.
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Jakoby,M.J., Heim,M.A. and Weisshaar,B.
TITLE Use of a gateway compatible vector for transient plant transfection
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4462)
AUTHORS Jakoby,M.J.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
FEATURES
source
1. .4462
/organism="Transfection vector pBTdest"
/mol_type="genomic DNA"
/db_xref="taxon:225975"
promoter
31. .443
/notes="35S"
TATA_signal
421. .424
/notes="35S"
misc_recomb
456. .580
/notes="attR1"
gene
689. .1348
/genes="cat"
CDS
689. .1348
/genes="cat"
/codon_start=1
/product="chloramphenicol acetyl transferase"
/protein_id="CAD83080.1"
/db_xref="GI:29335743"
/translations="MEKKTIGYTTVDISQWHRKEHFEAFQSVQACTYNTQVOLDITAF
LTKVKKHKFYPAFIHILARLNAHPEPRMAMKDGELVIWDSVHPCTYVFBQTETF
SLIWSVHDDFROFLHYSDVACYGENLAYFPKGIENMFVSNPVSFTSFDLNV
ANMDFPAPVFTMGKYTTQGDKVIPLAIQVHNAVCDGFHVGRLNELQYCDQWQGG
A"
1690. .1995
/genes="ccdB"
1690. .1995
/genes="ccdB"
/codon_start=1
/product="control of cell death B protein"
/protein_id="CAD83081.1"
/db_xref="GI:29335744"
/translations="MQFKVITYKRESRYRLFVDVQSDIIDTPGRMWIPLASARLLSD
KVSRELYPVVHIGDESWMRTTDMASVPVSVIGEEVADLSHRENDIKNALNMFWGI"
2036. .2160
/notes="attR2"
misc_recomb
2168. .2463
/genes="nosT"
2168. .2463
/genes="nosT"
gene
2606. .3466
/genes="amp"
2606. .3466
/genes="amp"
/codon_start=1
/product="beta lactamase"
/protein_id="CAD83082.1"
/db_xref="GI:29335745"
/translations="MSIQHFRVALIPFFAFCPLVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILDSFRPEELFPPMTSTFKVLICGAVLSRIDAGQQLGRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGKELTAFTHMNGDHTRL
DRWPELNEAI PNDERDTTPVAVATITLKGELTGLASRQQLIDMEADKVGPL
LRSLPAGWFIADKSGAGERGSGIITAAALGPDGKPSRIIVITGTSQATMDERNRQIA
EIGSLIKHW"
BASE COUNT 1223 a 995 c 1065 g 1179 t

```



```

source
1. .25
/organism="unknown"
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 2
LOCUS AR163180 25 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6270969.
ACCESSION AR163180
VERSION AR163180.1 GI:16233689
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 9 07-AUG-2001;
FEATURES Location/Qualifiers
source
1. .25
/organism="unknown"
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 3
LOCUS AX491648 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 9 from Patent EP1227147.
ACCESSION AX491648
VERSION AX491648.1 GI:22324156
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 9 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES Location/Qualifiers
source
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 4
LOCUS AX498619 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 9 from Patent EP1229113.
ACCESSION AX498619
VERSION AX498619.1 GI:23343416
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 9 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES Location/Qualifiers
source
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

RESULT 5
LOCUS BD131335 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131335
VERSION BD131335.1 GI:23226280
KEYWORDS JP 2002500861-A/9.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination sites.
JOURNAL Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PR 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source
1. .25
/organism="Unknown".
FEATURES Location/Qualifiers
source
1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 5 a 4 c 4 g 12 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTGTACAACTTGT 25
Db 1 GTTCAGCTTTTGTACAACTTGT 25

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 21:07:03 ; Search time 601 Seconds
(without alignments)
1701.732 Million cell updates/sec

Title: US-10-055-001A-4

Perfect score: 25

Sequence: 1 gttcagctttttgtacaaactgt 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:

2: gb_hgt:

3: gb_in:

4: gb_om:

5: gb_ov:

6: gb_pat:

7: gb_ph:

8: gb_pl:

9: gb_pr:

10: gb_ro:

11: gb_sts:

12: gb_sy:

13: gb_un:

14: gb_vi:

15: em_ba:

16: em_fun:

17: em_hum:

18: em_in:

19: em_mu:

20: em_om:

21: em_or:

22: em_ov:

23: em_pat:

24: em_ph:

25: em_pl:

26: em_ro:

27: em_sts:

28: em_un:

29: em_vi:

30: em_htg_hum:

31: em_htg_inv:

32: em_htg_other:

33: em_htg_mus:

34: em_htg_pln:

35: em_htg_rcd:

36: em_htg_mam:

37: em_htg_vrt:

38: em_sy:

39: em_htgo_hum:

40: em_htgo_mus:

41: em_htgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AR124529 Sequence
2	25	100.0	25	6	AR163180 Sequence
3	25	100.0	25	6	AX491648 Sequence
4	25	100.0	25	6	AX498619 Sequence
5	25	100.0	25	6	BD131335 Recombina
6	25	100.0	35	6	AX684690 Sequence
7	25	100.0	1846	6	AX703501 Sequence
8	25	100.0	4462	12	VFO551314 Transfect
9	25	100.0	5148	6	AX306327 Sequence
10	25	100.0	9019	12	AF408413 Binary ve
11	25	100.0	9019	12	AF408413 Binary ve
12	25	100.0	11005	12	AY196824 PiggyBac
13	25	100.0	11005	12	AY196824 PiggyBac
14	25	100.0	12677	12	AY196825 PiggyBac
15	25	100.0	12677	12	AY196825 PiggyBac
16	25	100.0	12789	6	AX590202 Sequence
17	25	100.0	13274	6	AX356862 Sequence
18	25	100.0	13990	12	AF541939 His-3 int
19	23.4	93.6	25	6	AR124530 Sequence
20	23.4	93.6	25	6	AR163181 Sequence
21	23.4	93.6	25	6	AX491649 Sequence
22	23.4	93.6	25	6	AX498620 Sequence
23	23.4	93.6	25	6	BD131336 Recombina
24	22.6	90.4	25	6	BD131368 Recombina
25	22.4	89.6	25	6	AR124535 Sequence
26	22.4	89.6	25	6	AR163186 Sequence
27	22.4	89.6	25	6	AX491654 Sequence
28	22.4	89.6	25	6	AX498625 Sequence
29	22.4	89.6	25	6	BD131341 Recombina
30	22.4	89.6	18691	12	CVE311874 Cloning v
31	22.4	89.6	18691	12	CVE311874 Cloning v
32	21.8	87.2	25	6	AX269136 Sequence
33	21.8	87.2	51	6	AX525413 Sequence
34	21.8	87.2	51	6	AX525421 Sequence
35	21.8	87.2	51	6	AX525429 Sequence
36	21.8	87.2	51	6	AX525456 Sequence
37	21.8	87.2	145569	5	AL935194 Zebrafish
38	21.2	84.8	25	6	BD131369 Recombina
39	20.8	83.2	25	6	AR124531 Sequence
40	20.8	83.2	25	6	AR124536 Sequence
41	20.8	83.2	25	6	AR163182 Sequence
42	20.8	83.2	25	6	AR163187 Sequence
43	20.8	83.2	25	6	AX269137 Sequence
44	20.8	83.2	25	6	AX491650 Sequence
45	20.8	83.2	25	6	AX491655 Sequence

ALIGNMENTS

RESULT 1
AR124529
LOCUS AR124529 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6171861.
ACCESSION AR124529
VERSION AR124529.1 GI:14109890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 9 09-JAN-2001;
FEATURES Location/Qualifiers